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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:	Requester's Full Name:		Examiner #:	Date:
Import Annone search Is submitted, please prioritize searches in order of need.	Art Unit: Phone N	Number 30	Serial Number:	Dinna Didi
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject mater to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract. Title of Invention: Inventiors (please provide full names):	Mail Box/and Bidg/Room Location	n: <u>L. 8 EM J.//</u> Res	ults Format Preferred (circle):	PAPER DISK E-MAIL
Include the elected species or structures, keywords, synonyms, actonyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract. Title of Invention: Inventors (please provide full names): Earliest Priority Filing Date: *For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number. **STAFF USE ONLY** Type of Search Na Sequence (9) STAFF USE ONLY* Type of Search Na Sequence (9) Dialog Searcher Penos #: Searcher Penos #: Searcher Penos #: Bibliographic Liftgation Levis/Nexts Sequence Systems Sequence Species	If more than one search is subm	nitted, please prioriti	ze searches in order of ne	ed.
Earliest Priority Filing Date: *For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number. STAFF USE ONLY Type of Search NA Sequence (*) Searcher: NA Sequence (*) Searcher Please Sincure (*) Outstel/Orbit Date Searcher Pleded Up: Bibliographic Lingation Lexis/Nexts Searcher Free & Review Time: Fulltext Sequence Systems Lingation Lexis/Nexts Sequence Systems Fulltext Sequence Systems	Include the elected species or structures, k utility of the invention. Define any terms	keywords, synonyms, acroi that may have a special m	nyms, and registry numbers, and concerning. Give examples or relevant	ombine with the concept or
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Earliest Priority Filing Date: *For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number. STAFF USE ONLY Type of Search NA Sequence (**) Searcher Per None (**) Searcher Plone (**) Searcher Plone (**) Searcher Plocked Up: Bibliographic Date Searcher Pleked Up: Bibliographic Searcher Pleked Up: Searcher Pleked Up: Bibliographic Date Searcher Pleked Up: Searcher Pleked Up: Bibliographic Date Searcher Pleked Up: Bibliographic Date Searcher Pleked Up: Bibliographic Date Searcher Pleked Up: Bibliographic Searcher Pleyed Review Time: Fulltext Sequence Systems	Inventors (please provide full names): _			
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PTO-1590 (1-2000)

GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.

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US-08-628-417-6
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2, 1	Sequence 10, Appl	Sequence 66, Appl	Sequence 19, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 2131, Ap	Sequence 5, Appli	126	$\overline{}$	9	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 1, Appli	<u>, , , , , , , , , , , , , , , , , , , </u>	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-08-232-463-14/c

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52

•1		
	US-08-232-463-14	c
	CLONE: pTZgpt-Fls	٠.
	IMMEDIATE SOURCE:	٠.
	TOPOLOGY: linear	٠.
	STRANDEDNESS: single	٠.
	acio	٠.
	LENGTH: 7218 base pairs	٠.
	SI	٠.
	INFORMATION FOR SEQ ID NO: 14:	٠.
	TELEX: 899149	٠.
	TELEFAX: (703)683-4109	٠.
	TELEPHONE: (703)836-9300	٠.
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	RATION NUMBER: 29,7	٠.
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	FILING DATE: 26-AUG-1991	٠.
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	FILING DATE:	٠.
	APPLICATION NUMBER: US/07/935,313	٠.
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	CLASSIFICATION: 435	٠.
	FILING DATE:	٠.
	APPLICATION NUMBER: US/08/232,463	٠.
	LICATION DATA:	٠.
	SOFTWARE: PatentIn Release #1.0, Version #1.25	٠.
	OPERATING SYSTEM: PC-DOS/MS-DOS	٠.
	COMPUTER: IBM PC compatible	٠.
	MEDIUM TYPE: Floppy disk	٠.
	COMPUTER READABLE FORM:	٠.
	31	٠.
	COUNTRY: USA ,	٠.
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	ADDRESSEE: Foley & Lardner	
	CORRESPONDENCE ADDRESS:	

Query Match

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                                                                                                                      TELEFAX: 410-671-2534 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GG)
CITY: ABERDEEN PROVING GROUND
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                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 240 bases
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ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
                   TOPOLOGY: 1
MOLECULE, TYPE:
                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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      HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14,
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                     TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1185 AATATGAACTTAATCTTATTGTTAGTTTACCAGCACCAGAGAAACCAAAAGGAAAACCAG 1244
                                                                     MOLECULE TYPE:
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SECRETED PROTITITLE OF INVENTION: ENCODING THEM NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
                                                                                      TOPOLOGY:
                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.ZIP: 02140
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                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                       Sprunger, Suzanne A. RATION NUMBER: 41,323
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                                                                                                                  nucleic acid
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87 CambridgePark Drive
                                                                                                                                    2447 base pairs
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Spaulding, Vikki
Agostino, Michael
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LaVallie, Edward R.
                                                                                                                                                                                      (617) 876-5851
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Pred.
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Pred. No. 0.00054;
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US-08-973-462-2
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1996-06-12
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Best Local :
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TYPE: DNA
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  ATTTTGGAGGAAAGTCAAGTTAATGACGATATTTTTAATAGTTTAGTAAAAAAGTGTTCAA
                                     GATGTTCAGATGAATGAGAGTTTTGATAATAATCATAGCATGTCACGAGCAAAGAAGAAA 4228
                                                                                                                      GAGAATGTGATTAATGACGATGACATTGCTGAAGCTAATCCACTACCAGATGAAAATAAT 4168
                                                                                                                                                                    AATAATATTGGACAAAATTCAGAAAAACAAGAAAGTGTATCAGAAAATGTACAAGTCAGT
                                                                                                                                                                                                         GAAAGTATCCTTGCTGATAAGAGATTGGATGAATTTGAAACGTATAATGTTGATGAAATT 4108
                                                                                                                                                                                                                                                     GAAAATATCTTATTAAGTAATATAGAAGAACCAAAAGAAAATATTATTGACAATTTATTA 468
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                                                                                                                                                                                                                                                                                                                                                                             ACTGAACTTGCTACAGACTCGGGAAATGATAGCAATTCAACAGAATCCGACATTCAATCG 3988
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Pred. No. 0.0036;
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US-09-410-464-9

GENERAL INFORMATION:

APPLICANT: Strauss et al.

TITLE OF INVENTION: Floral homeotic genes for manipulation TITLE OF INVENTION: poplar and other plant species. FILE REFERENCE: 53375 CURRENT APPLICATION NUMBER: US/09/410,464 CURRENT FILING DATE: 1999-10-01 EARLIER APPLICATION NUMBER: 09/287,700

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flowering

Sequence 9, Application US/09410464 Patent No. 6395892

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CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
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APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
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EARLIER APPLICATION NUMBER: FR 95/07007
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                                                                                                                GATGTTCAGATGAATGAGAGTTTTGATAATAATCATAGCATGTCACGAGCAAAGAAA 4228
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CAAGAACAACAACAATGTTGAAGAAAAAGTTGAAGAAAGTGTAGAAGAAAATGA
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Pred. No. 0.0037
0; Mismatches 2:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan,
STREET: 5370 Manhattan Circle, Suite 201

STATE: CITY: Boulder

Colorado

TITLE OF INVENTION: Retrotransposon NUMBER OF SEQUENCES: 51

and Methods

APPLICANT:

Zou,

Sige

Voytas, Daniel F.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 348; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4888
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                                                                                                                                                                                                                                                        TGAATATGAAGAGGGATCAGTAATATTTAGGTTTATATGTTGATGATATTCTTATGGT 5067
                                       TTATATTTTATCTCAAGAAAATTTCTCAAGAAATTTACTTAAGGATTTCAAACTAGATGA 5247
                                                                                                                            TAAAGTGTTTGGTGAAATATCAAATTATCTTGGTATTGAATTTCGTAAAACCGAATCTGG
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TTACCTTCTTCTCAGTCGAAATATGTTGCAGATATTCTTGAGCAGACTAGACTTACTGA
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                                                                                                                                                                        TGGTGATGACATTGATGTTTCAGTCTTGAAGACAAAGTTGGCTAGACGATTTGAAAT
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Pred. No. 0.0054;
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RESULT 7 US-08-771-602D-1

Sequence 1, Application US/08771602D Patent No. 5976795

GENERAL

INFORMATION:

밁 Qγ US-08-771-602D-1 Matches 241; Query Match TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TOPOLOGY: not re MOLECULE TYPE: DN/ HYPOTHETICAL: NO FEATURE:
NAME/KEY:
LOCATION: 4661 GGCAACAGACAAAAGGAAAAATTGGATTATGACCCTTTTAGTGTTAGTTCACCCTGTTATA 4720 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS FILING DATE: 31-JAN-1996 ATTORNEY/AGENT INFORMATION: SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: FEATURE: TELECOMMUNICATION INFORMATION: FEATURE: FEATURE: FEATURE: ORIGINAL SOURCE: ANTI-SENSE: PRIOR APPLICATION DATA: LOCATION: 2852..4827
OTHER INFORMATION: /function= "integrase region coding
OTHER INFORMATION: region of Ty5-6p" LOCATION: 6352..60 OTHER INFORMATION: NAME/KEY: misc_feature LOCATION: 6352..6602 OTHER INFORMATION: ORGANISM: Saccharomyces paradoxus STRAIN: NRRL Y-17217 APPLICATION NUMBER: US 6 FILING DATE: 31-JAN-1996 Local Similarity NAME/KEY: misc_feature LOCATION: 2852..4827 OTHER INFORMATION: TYPE: nucleic acid FILING DATE: 20 CLASSIFICATION: NAME/KEY: misc_feature LOCATION: 1228..1478 LOCATION: NAME/KEY: STRANDEDNESS: TELEPHONE: REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER: APPLICATION NUMBER: COUNTRY: GCCCAAGGACATACTCAAAAAGGCTGGTATTGACTATCAAGAAACTTTTTGCACCAGTCATT 5040 80303 Ferber, Donna M. USA Conservative Ö not relevant misc_feature 1228..6602 1441..6321 CDS (303) 499-8080 20-DEC-1996 N: 435 DNA (genomic) double 0.8%; 45.2%; /function= /product= /function= /function= us 60/010,869 US/08/771,602D 0; Score 54.6; DB 2; Pred. No. 0.0077; Mismatches **"**3' "retrotransposon" . 5 LTR LTR of Ty5-6p of 289; Ty5-6p" Length 6660; Indels ω Gaps

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SOFTWARE: Patentin V
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Voytas, Daniel F.
APPLICANT: Gai, Xiaowu
APPLICANT: Gai, Xiaowu
TITLE OF INVENTION: Transposable Element Protein that Directs
TITLE OF INVENTION: Integration to Specific Chromosomal Sites
FILE REFERENCE: 2-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/232,446B
CURRENT FILING DATE: 1999-01-15
PRIOR APPLICATION NUMBER: US 60/071,383
PRIOR FILING DATE: 1998-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                     .TYPE: DNA
ORGANISM: Saccharomyces paradoxus
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1441)..(6318)
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                             4721 GATCTTGTGACTATAAGATTATTGACAATAATAGGTTGTGAATTAGGAATGACAATTCAA 4780
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CATTTAGACGTCGAGTCGGCGTATCTAAATGCCTCTATTACTCATTCAAATCCAATTTAT 4840
                                                                                     CGATATGACTCTGTTAGATTATTTCTGGCCCTTGCTAGCTGCCTCAAACTAATAGTATAT 5100
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; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 151

; LENGTH: 3275

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-370-838-151
Db
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APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: CUMPOUNDS FOR THERAPY AND DIAGNOSIS (
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USI
FILE REFERENCE: 210121.475C1
CURRENT APPLICATION NUMBER: US 09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6444425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                     1331 GGTGAAAAAGAAAAAGAAAAAGAAAAACTTC 1362
                                                                                                                        1271 AAGAAGAACCTGAAATCAAGAAAGAGAAATAAGAAACATCCAAAATCAGATAACGATAAA 1330
                                                                                                                                                                                                         1211 TTACCAGCACCAGAGAAAACCAAAAGGAAAACCAGAGGAGAACTCACTGGAACAATCTCAA 1270
3241 АААААААААААААААААААААААААААААСТС 3272
                                                                                                                                                                  5458 AAAGTTGACAAATTCCTCGGTCTTAACATTAATCAATTTTCAAATGGAGACAT 5510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5141 GAAATATCAAATTATCTTGGTATTGAATTTCGTAAAACCGAATCTGGTTATAT 5193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4841 GTCTTTCCTCCTAAATCAGTACCTTTGAAGAAAAACCATTGTTGGTTATTGAAACGTTCT 4900
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                              AAAATATATGACAGGGTTAAGCAGAAACTAACGAAGTTATACTCAATGAAGGATCTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGTTATTGATAATTTTGTGGATCAATTGAGAGATCATTTTGAAGTTAAAGTGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATCAGTAATATTTAAGGTTTATATGTTGATGATATTCTTATGGTTGGAAGTTCACAA 5080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGATTGGTTTTCGTCGACATGAAGGCGAACATGGCTTAT---ACTTTCGTTCCACATCT 5337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTATGGGTTAAAACAGTCGGGTTTGGAATGGTATCACACTATCAAAAGAGTATTGGAA 4960
                                                                                                                                                                                                                                                                91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reed, Steven G.
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                          0.8%;
                                                                                                                                                                                                                                                       Score 54.4; DB 4; Length 3275;
Pred. No. 0.0069;
0; Mismatches 61; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR THEIR USE
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RESULT 10 US-09-797-906-1

GENERAL

INFORMATION:

APPLICANT:

Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M.

BEASLEY

Sequence 1, Application US/09797906 Patent No. 6329188

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001151C1P
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1798
TYPE: DNA
ORGANISM: Human
                                                                                                                                 REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stewart, Thomas APPLICANT: Flores, Maria V APPLICANT: O'Sullivan, Will
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.24 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
   MOLECULE TYPE:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1197 ATCTTATTGTTAGTTTACCAGCACCAGAGAAACCAAAAGGAAAACCAGAGGAGAACTCAC 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
CITY: P
                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Vira
                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 06-Jul-1995
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                    TOPOLOGY:
                                                                                                                   TELEFAX:
                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                LENGTH:
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                                                                                                                                                                                                 Mitchard, Leonard
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                                                                 8920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Nixon & Vanderhye PC 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                  703-816-4100
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                    linear
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genomic
                                single
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                                                    ; ORGANISM: Plasmodium US-09-150-741-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6183996 TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09150741 Patent No. 6183996
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Best Local Similarity
                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILLING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
                                                                                                                                                                                                   EARLIER FILING DATE: 1995-07-06 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                               TYPE: DNA
                                                                                                                         LENGTH: 8920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4233 CATTTGAGAAAGAAGTTAACGAAAAAATTGCTGGTACTAAACATTCACTTGATACAACTG 4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6031 TATGAATTGTTCTAATTATAATAATGCTAGTGCATTTGTAAATGGAAAGGATAGAAATGA 6090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACATCACATTCAACTAATGATCATTTATATTTTAGATAATTTTAATACATCAGATGAAGA 5850
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Score 53.2;
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Query Match

DB

Length 8920

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5766597
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6151 TTTAAACA 6158
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                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4293 ATCCAAGA 4300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5851 AATAGGGAATAATAAAAATATGGATATGTATTTATCTAAGGAAAAAAGTATATCTAATAA 5910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3820 AGTTTCT---CAAGAGGGAAGAATACTTAATGAACAAACTGATATAGTTGATACTGTTGC 3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Paoletti, Enzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5791 AACATCACATTCAACTAATGATCATTTATATTTAGATAATTTTAATACATCAGATGAAGA 5850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3877 TAAAGTTATTGAGAATGAAAAATCTCTCTATTAATTCATTAGATGATCATACTGAACT 3936
                                                                                                                                                                                                                                                        STATE: N
                                                                                  FILING DATE:
                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                CLASSIFICATION:
                                                                                APPLICATION NUMBER: US/08/257,073 FILING DATE: 09-JUN-1994
                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                CITY: New York
                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08257073
                                                                                                                                                                                                                                                                            New York
                                                                                                                                                                                                                                                                                                          E: Curtis, Morris & Safford, P.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                             de Taisne, Charles
Tine, John A.
                                                                                                                                                                                                                                                        UNITED STATES OF AMERICA
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                                                                                                                                                                                                Floppy disk
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US-09-134-001C-322
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                                                                                                                                                                                                                                                                                                                SEQ ID NO 322
LENGTH: 30549
                                                                                                                                                                          Matches 187;
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lynn Dou
                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 322, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local Similarity 57.3%;
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
13985 AGCGACAAACTTTAACTGATACTATAAATCACTCTCCAAACATCAATTCAGTGAATCAAG 14044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 840-071
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO:
                                                                                 13925 AAGTTGCTAAACAACAAGCACTTAATCATTTAAATACCTTAAATGATTTAAACGATGCTC 13984
                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                             TYPE: DNA
                                      3939 CTACAGACTCGGGAAATGATAGCAATTCAACAGAATCCGACATTCAATCGAAAAATGAAA 3998
                                                                                                                   3879 AAGTTATTGAGAATGAAAAAATCTCTCCTATTAATTCATTAGATGATCATACTGAACTTG 3938
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LENGTH: 2223 base pair
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APPLICATION NUMBER: [
FILING DATE: 18-MAR-1
PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 45
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(212) 840-0712
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Pred. No. 0.021;
0; Mismatches 70; Indels
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                                                                                                                                                                                       Score 52; DB 4; Length 30549; Pred. No. 0.044;
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CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
LENGTH: 1447
TYPE: DNA
ORGANISM: Glycine max
US-09-443-041A-27
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Search completed: April 27, 2003, 16:51:08 Job time: 575 secs
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8%;
Best Local Similarity 55.2%;
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14285 ATCTAAATGGTAATGACAAATTGGCTGAAGCTAAAAGAGATGCTAATACAAC 14336
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                                                                                          1434 A 1434
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                                                                                                                                                                                 1318 AGATAACGATAAAGGTGAAAAAGAAAAAGAAAAAGAAAAACTTCACTGGAATGAAAAAC 1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.4; DB 4; Length 1447; Pred. No. 0.025; O; Mismatches 81; Indels 0.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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seq length: 2000000000
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6426
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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21 21 21 21 21 21 21 21 21 21 21 21 21 2	DB
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1348	951	770	138	1672	1912	938	936	936	936	936	936	938	936	936	936	936	936	690	3604	9850	469	1308	974	454	879	5611	1483	1249	1385	392	392	392	392	
21	21	21	21	21	21	22	22	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	
AAA57983	AAA58017	AAA57964	AAA57937	AAA57950	AAA57952	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254	AAF58252	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254	AAF58252	AAA57951	AAA57946	AAA58018	AAA57994	AAA57949	AAA57992	AAA57967	AAA57991	57	579	579	579	579	AAA57924	579	AAA57934	
1348 bp Candida al	951 bp Candida alb	770 bp Candida alb	Candida albicans s	1672 bp Candida al	1912 bp Candida al	Oligonucleotide Dl	Oligonucleotide D2	Oligonucleotide D2	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D2	Oligonucleotide D2	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1	690 bp Candida alb	3604 bp Candida al	9850 bp Candida al	469 bp Candida alb	1308 bp Candida al	974 bp Candida alb	Candida albicans m	879 bp Candida alb	5611 bp Candida al	1483 bp Candida al	1249 bn Candida al	1385 bp Candida al	albicar	Candida albicans s	albicar	Candida albicans s	

ALIGNMENTS

RESULT

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FT	7 17 14 14 14 14 14 14 14 14	1 H H I	1 H H H	1 11 11 1	FT	XX SO	X X X	X Z	X X	X X E	XX	XX AC	AAA5791 ID AA
repeat_unit	polyA_signal	TATA_signal	TATA_signal	repeat_unit	Key LTR	Candida albica	genetic vaccine	stop codon supp	gag gene; group	Candida albica	11-OCT-2000 (AAA57920;	AAA57920 ID AAA57920 stand
275280 .	/*tag= d /standard name= "TATA box" 201206 /*+52-		<pre>/rpt_type= INVERTED /note= "Imperfect 6 bp repeat" 120125</pre>	/*tag= a 1.6d 1.6d /*tag= b	Location/Qualifiers 1280	albicans strain hOG1042.	genetic vaccine composition; immunogenic; transgenic animal; ds.	reverse transcriptase; RNaseH; pseudoknot; readthrough translation; stop codon suppression; gene delivery; gene therapy vector:	gag gene; group antigen; polyprotein; pol; asparate protease; integrase;		(first entry)		AAA57920 standard; DNA; 6426 BP.

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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                   TATA_signal
                                                                                                                        TATA_signal
                                                                                                                                                                       repeat_unit
                                                                                                                                                                                               LTR
                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                        primer_bind
                                               polyA_signal
                       repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stop codon suppression mediated by pseudoknot formation in the mRNA"

/codon= (seq:"ctg", aa:Ser)
/note= "12 serine residues in the gaq-pol residues
                                                                                                                                                       /*tag= p
6147..6152
/*tag= q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type= INVERTED
/note= "Imperfect 6
281..291
                     /*tag= t
6421..6426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "This site in binding site minus-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              readthrough protein" /note= "The gag-pol readthrough protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Gag (group antigen) protein"
/codon= (seq:"ctg", aa:Ser)
/note= "5 serine residues in the gag pr
                                                                                                                                                                                                                                                                                                                                                      /note= "Polypurine tract 2 (PPT2)" complement (3455..3465)
                                                                                                                                                                                                                                                                                                                                                                                               3455..3465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1373..6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "The RNA corresponding to this region forms a pseudoknot, allowing gag ORF stop codon suppression and translation of the gag-pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381..1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498..6103
                                             /standard name= 6347..6351
                                                                                                                                                                                                                                                            complement (6136..6146)
                                                                                                                                                                                                                                                                                                6136..6146
                                                                                                                                                                                                                                                                                                                                                                                                        (RT) and RNaseH"

/codon= (seq:"ctg", aa:Ser)
/note= "7 serine residues in the pol protein are encoded
by this non-standard Ser codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= (pos:1367..1372, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Gag (group antigen)-pol (polyprotein)
                                                                                   6331..6336
                                                                                                                        6266..627
                                                                                                                                    /rpt_type= INVERTED
/note= "Imperfect 6 bp repeat"
                                                                                                                                                                                               6147..6426
                                                                                                                                                                                                                                                                       /note= "Polypurine tract 1 (PPT1)"
                                                                                                                                                                                                                                               /*tag=
/rpt_type= INVERTED
                                                                                                /standard name=
                                                                                                                                                                                                                                                                                    /*tag=
           /*tag=
                                                                        /*tag=
                                                                                                             *tag=
                                                                                                                                                                                                                                   "This site in the corresponding RNA is a primer
                                                                                                                                                                                                                                                                                                          "This site in the corresponding RNA is a primer binding site for reverse transcriptase-mediated plus-strand DNA synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by this non-standard Ser codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon"
                                                                                                                                                                                                           binding site for reverse transcriptase-mediated plus-strand DNA synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       readthrough protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Pol (polyprotein), comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease,
                                                                                                   "TATA box'
                                                               "TATA box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the corresponding RNA is a primer for reverse transcriptase-mediated DNA synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         integrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the gag protein are encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                         reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of.
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121 ataaataagggtatgaaataccaacatcccagaatatcaacgagatagaagggaggagtt 180

180

61 gaatggaaaatttttccatcacacatcaggtgatgacagaactaaactatattgtgtagt 120

0;

gaatggaaaatttttccatcacacatcaggtgatgacagaactaaactatattgtgtagt 120

181 tcaatatatcttgtgaataattaacttcgttctaattcactatacacaactagacgtgt 240 121 ataaataagggtatgaaataccaacatcccagaatatcaacgagatagaagggaggagtt

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                                                                                                Matches 6425;
                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel retrotransposons from the yeast Candida albicans which have a copy number of 40-150, preferably 50-100 copies per genome. In particular, the invention relates to the novel C. albicans Tyl/Copia retrotransposon pCal (AAA57920), and to the integrated form of this retrotransposon, designated TCa2, and to the novel C. albicans retrotransposons 1-28. pCal was initially isolated from C. albicans retrotransposons 1-28. pCal was initially isolated from C. albicans hOG1042 and has a copy number of 50-100 copies per cell. It comprises identical 280 bp long terminal repeats (LTRs) and two open reading frames (ORFs). The first ORF encodes a gag (group antigen) protein, and the second ORF encodes a polyprotein (pol) consisting of an aspartate protease, integrase, reverse transcriptase (RT) and RMaseH. The gag and pol ORFs of pCal are in the same reading frame, separated only by
                                                                                                                                                                                                                                                                                    for the delivery and expression of a therapeutic, immunological or immunospenic molecule (e.g., an antigen) and may also be used for eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate transgenic animals, to detect the presence of Candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide sequences. The present sequence represents the C. albicans pCal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. T aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. T gas and pol ORFs of pCal are in the same reading frame, separated only a termination codon (TGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is mediated by the formation of a pseudoknot within the gag-pol mRNA. The retrotransposons of the invention can be used as vectors for in vitor or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 2B; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen, epitope or therapeutic agent, or presence of Candida in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200026397-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel retrotransposon expression vectors useful for antigen, epitope or therapeutic agent, or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB03126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1998;
                                                                                                                                                                                                                    Sequence 6426 BP; 2228 A; 1032 C; 1258 G; 1908 T; 0 other:
                                                                                                                                                                                                                                                                       retrotransposon.
                                                                                                                            Local Similarity
                         1 tgttggtttgtgcactattttgtgtcagaaactgatcaatgaaaatgatggttattatga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-365640/31
tgttggtttgtgcactattttgtgtcagaaactgatcaatgaaaatgatggttattatga 60
                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0106342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB03127, AAB03128
                                                                                                                         100.0%;
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                                                                                                                              Pred. No.
                                                                                                                                                  Score 6424.4;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poulter RTM;
                                                                                                                                                     DB 21; Length 6426;
                                                                                                       1.
                                                                                                       Indels
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                                                                                                       0,
                                                                                                       Gaps
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1320 1320	. acaatctcaaaagaagaacctgaaatcaagaaagagaaataagaaaca 	1261	Db VY
1260 1260	Tattgttägtttaccagcaccagagaaaccaaaaggaaaaccagaggagaactcactg 	200	0 dg (4
0 0	tgatcatcotgattatgotagattggttgacattccaagcaacaaatatgaacttaa 	14	y da
1140 1140	. tcaagctgacaatgatacatcagtactcccaagttgctctaccatagctgaagaaatg 	0 0	рb
1080	. gaaatcagaggctttaagtttgtttttgaatattcatgcctcatactactcaaagt 	0 0	оу Ор
1020 1020	 tgagtatgtccgtagtcttccaaatctcataggtcaagtcttgtacttcaatcatgtg 	9 9	Од
960	. ttgctgcaggtggaagagaaacttgaggaaatactctacaacacttcaaacgttgtcga 	901 901	Оy
900 .	gatettgetgaagtttgtaaaegttgaaeatgagttagtggtttgetätaaeetteeata 	4 4	Db Qy
840 840	. Cttaatcaaagctgcttatgatgctgttactaaatctaaagattataccattactagtaa 	ο ο ο	ДЬ ОУ
780 780	. tgataggitcagattgatcatgattictaagciaccamaagcacttgcaamaggaagcaaa 	NN	Db dy
720 720	aaggtagaaggtatttatttactggttggtgtttacaaatgtgtttacagtccatttt 	9. 9.	Dp Qy
660	<pre>ttaccccgatgttttggaatttttgcttgactataatcctaaagataaattcaaggttaa </pre>	0 0	Db VQ
600	gtoggtaatcagaaaagogtggataaatggaatgaagaatttaaatatttccacgttgc 	4 4	ду Дъ
540	atatcaaggctagattcaatatgcttttcataaaatttaatgacttacctaagttg 	00 00	dd Ao
480 480	. taacgaagggaaggtcatggaaagtgttgatcaagct 	NN	망 (5
420 420	gatagtttogaagtttgaaggtacagaatttcacaagatgagttccgcaaagaat 	. 36	da oy
360 360	aatcatttcgtcocaaattagcgttgtataaattcagtcotcagatttgtattattgat 		Qy da
300	cacgctcaatctcaggtaaagaaagtttatattccatcagattagaagtcgata 	24	Ф
240	. tcaatatatatcttgtgaataataacttcgttctaat	. 00	Db

2400	. aacgtctgttatagatgaacatacgggttacattgaaggaattattactaaagacagaaa	2341	Db
2400			Db
2340	tgagagaettcattgtgatactotcggtocatttaggtocgaaaataacaagtggtattt	2 2	dq
2340			Qy
2280 2280	atogaatgocaaacagagaagtoacaatcatcattcagaaagaaaagcotcgagaagaca 	222	g dd y
	<pre>gqtacttcacacttcaaaagagagtcttcaaaagattgctgattgtaaggtatgtctatt </pre>	216 216	o do Qy
2160	. trigatgicaaatcatatgtccattgagaaaatcttgttgttacaaaaataccagggtct	210	Db
2160		210	Dy
2100 2100	CCCATAT99a9tT9aaCaatT9CtaCCaaCT99a9ataagaaCgatatttataatttcca 	2 2	Db 29
2040	tagttctcgagcattaataaattctttgacggaggttgatgttttagatgttgaaatttc	198	Oy
2040		198	Db
1980	. ccaagatgacaaagataaatcaagtatgaatgaaatgtcagaatatcaagaacatgatta	192	pb 04
1980		192	
1920	. agaatctttagaatgtgattttgattatgatggtttggcagatatgttgtccaatgctaa	186	Db
1920		186	Qy
1860	. tactattattgcttcaaggaagaatgctgctgatctttatatgggtcctcaattcagtga	180	DF
1860		180	OA
	aggatttaatgttottattactaaagaatcagtgattgtatttaaccaaaa 		D Q
7	. tacattgtatttaccagaaagttcctttaatcttgtgagtttgaaacaaattgaagaacg 	168 168	D Q
1680	l agcagattgtattggtgatctaattatcagagtcggtattgtctcgatta	162	B 8
1680		162	
1620.	1 attgctgaalgttaaggacgcaacaattgaagtttctgttgctgatggtgctacattaga	156	₽ S
1620		156	
in in	taacaagtatctagtgtatgatactggtgccacaatatctgtt	150 150	B 8
1500	ttctcttaatgcttctt	144	₽ <i>9</i>
1500		144	
1440 1440	1 tgctgcttctattaattgtgtaatgaatatacattaattgcagcaaaaccacgtttccagt	138	Db Qy
1380	1 taacgataaaggtgaaaaagaaaaagaaaagaaaaacttcactggaatgaaaacagg	132	Qy
1380			Db

Qy 2401 gytaaasgaatttaattcaasgaattaattgatttaacgattaattgattaacgaattagggattaattgattaacgataaggt 246 2401 gytaatggattttaattcaacgattaattgattaagatcgattgatt	2401 ggtaanggatctctttaattcaacgattaaagatctggaataatcggtttaacggttaaggt 24 ggtaatggatctttaattcaacgattaaggt 24 ggtaatggatctttaattcaacgattaaggtttcagttgattattaacgattaaggt 24 ggtaatggatctttaacgattaaggttgttgttattattcaacgattaggttgttgttgttattaggtgagttaggattatttaatggattaggttgtt														_					
401 gytaaagyattottottaattoaacyattaaagatctygaataatsctygtttaacyattaacyataagyt 246	401 ggtaaaggatctctttaattoaacgattaaggattaaattggtttaacggattaaggt 2466	Qy	Qy Db	Оу	Qу	Qy Db	Qy da	₽ ^V	Фр	. Qy	Qу	Qy Db	Qy Db	Qy Db		Qy Db	Оу	Qу	Оу	Qy Db
	graaaggatctcttaattcaacgattaaagatctggaataatcggtttaacgataaggt 2466 graacgatcattcagaaggatcgattaacgattaaggatctccacagagttlillillillillillillillillillillillilli	48	42 42	36	30	24	18	12	0 0	0 0	9 9	88	ထ ထ	7	7	9 9	ഗഗ	52	4 6	40
		, gaatetaetgeteaggttggaetateacaeceaaececagaetggtaeteeegettegga 354	CCTATTACAAACCACACAAAGGACGCCCCTTCCATCCAGGGGGGGG	coggtgtctaaacctcotcaacttggtaccgagacttcagtaatagggaagtctaaaga 342 	gaagtaaaatcggatgagaatcctaaacccagtctccacgagctaacacctggggataa 336 	aatcocgatgatttttctaaccctcttcaactaactgaagaatcacacgatatggtatc 33 	acgggtaacagttctaacgaatatgttataaatgatgatccagtacagattaccattga 324 	gacgtgatgcacatgcccaaagagtcatattcagttcag	ctgggcgctcagtacgaggtacgcggaacatatgtggaaagtgaatatgacaatacaaa 312 	ttatccactacacctatgtcacacattgttcctatggctgaaggtatccagggaaggca 30	cttagccctaatgtccgtatattgcgaagctatgaggttattaactcctatctcaaaaa 30 	tacgctagcgattgttttagttattacgtgttgctaaaaaatatgcggtgtgatattat 294 	cgttacggagttacatcaactaaaggagctccttcatcgatcatgggtgctgtgattgg 288 	tacoggittccitttgccatogattgigtcgitacatttagiaatgccatcgaaaagaa 282 	cgttcactcaagggacaaaccccttatggttgctattatcaattaagtgagggaaattt 276 	otcaagttgatttattatgtgattcaatattctattacaatgatcaaccacactccacg 270	gttaataaattgattttacaacagatttacaggatcgttgtgacacttggtccacaaat 264 	ggtatttggagggagactatagcggcatatctgcctgagcttaatggtctcgccgaggt 258 	gcatacttcagaagtgataatgctcctgagttcccacaaccttctgatttagctgagtt 252 	gtaaaggatotottaattoaacgattaaagatotggaataatoggtttaaogataaggt 246

gagatchacatdactyptcaggatcagatcattcagtgctgagactgatcagacaga
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AAA57936 standard; DNA;

10-OCT-2000 entry)

Candida albicans strain p36 TCa2 retrotransposon ú region

Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat; LTR; gag gene; group antiqen; polyprotein; pol; asparate protease; integ reverse transcriptase; RNaseH; pseudoknot; readthrough translation; stop codon suppression; gene delivery; gene therapy vector; genetic vaccine composition; immunogenic; transgenic animal; ds.

Candida albicans strain p36

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CC mediated by the formation of a pseudoknot within the gag-pol mRNA.
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immunogenic molecule (e.g., an antigen) and may also be used for eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel retrotransposon expression vectors useful for expressing an antigen, epitope or therapeutic agent, or detecting genes or the presence of Candida in a sample - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic vaccine composition; immunogenic; transgenic animal; ds
                                                                                                          The retrotransposons of the invention can be used as vectors for in vitro or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1998;
30-OCT-1998;
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98US-0106342
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RESULT
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Best Local Similarity
Matches 390; Conserv
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                                                                                                                                                                                                                                  Candida albicans strain ATC-1.
                                                                                                                                                                                                                                                            gag gene; group antigen; polyprotein; pol; asparate protease; integrase; reverse transcriptase; RNaseH; pseudoknot; readthrough translation; stop codon suppression; gene delivery; gene therapy vector; genetic vaccine composition; immunogenic; transgenic animal; ds.
                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2000
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                                                                                         30-OCT-1998;
30-OCT-1998;
                                                                                                                                         01-NOV-1999;
                                                                                                                                                                                                                                                                                                                          Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat; LTR;
                                                                                                                                                                                                                                                                                                                                                                                                                           AAA57927;
                                                          (JANC ) JANSSEN PHARM NV
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                           De Backer
                                                                                         98CA-2249046
98US-0106342
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                                                                                                                                                                                                                                                                                                                                                         strain ATC-1 TCa2 retrotransposon
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Pred. No. 6.9e-70;
"""matches 2;
                           Nelissen BJM,
                           Poulter
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CC form of this retrotransposon, designated TGA2, and to the novel C.
CC albicans retrotransposons 1-28. pCal was initially isolated from C.
CC albicans hGG1042 and has a copy number of 50-100 copies per cell. It
CC comprises identical 280 bp long terminal repeats (LTRS) and two open
CC reading frames (ORFs). The first ORF encodes a gag (group antigen)
CC protein, and the second ORF encodes a polyprotein (pol) consisting of an
CC aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The
CC gag and pol ORFs of pCal are in the same reading frame, separated only by
CC the occasional readthrough suppression of the pol ORF occurs through
CC the occasional readthrough suppression of the gag-pol mRNA.
CC The retrotransposons of the invention can be used as vectors for in
CC vitro or in vivo transformation and expression. They can thus be used
CC for the delivery and expression of a therapeutic, immunological or
CC eliciting an immunological response in a host organism. They are
CC undesirable. Additionally, the retrotransposons may be used to generate
CC transgenic animals, to detect the presence of Candida in a sample, to
CC sequences. Sequences AAA57923-A57936 represents TCa2 retrotransposon 5'
CC regions from a variety of C. albicans strains.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen, epitope or therapeutic agent, presence of Candida in a sample -
                                                                                                                                                                                                                                                                                                                     Sequence 392
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                                         gaatggaaaatttttccatcacacatcaggtgatgacagaactaaactatattgtgtagt 120
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                     BP; 136 A; 56 C;
                                                                                                                                                                                                                                    6.1%;
                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                    Score 388.8; DB : Pred. No. 6.9e-70
                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                     G;
                                                                                                                                                                                                                                                                                                                     128 T; 0 other;
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392
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RESULT AAA57928

DЪ QY Дb QУ В QyВр

392 BP

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Matches
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                                                                                                                                                                                                                 for the delivery and expression of a therapeutic, immunological or immunopenic molecule (e.g., an antigen) and may also be used for eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or
                                                                                                                                                                                                                                                                                                          aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. T gag and pol ORFs of pcal are in the same reading frame, separated only a termination codon (TGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is mediated by the formation of a pseudoknot within the gag-pol mRNA. The retrotransposons of the invention can be used as vectors for in vitro or in vivo transformation and expression. They can thus be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel retrotransposons from the yeast Candida albicans which have a copy number of 40-150, preferably 50-100 copies per genome. In particular, the invention relates to the novel C. albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated form of this retrotransposon, designated TCa2, and to the novel C. albicans retrotransposons 1-28, pCal was initially isolated from C. albicans h0G1042 and has a copy number of 50-100 copies per cell. It
                                                                                                                                          undesirable. Additionally, the retrotransposons may be used to generate transgenic animals, to detect the presence of Candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide sequences. Sequences AAA57923-A57936 represents TCa2 retrotransposon 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                        albicans hog1042 and has a copy number of 50-100 copies per cell. It comprises identical 280 bp long terminal repeats (LTRs) and two open reading frames (ORFs). The first ORF encodes a gag (group antigen) protein, and the second ORF encodes a polyprotein (pol) consisting of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Fig 9;
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30-OCT-1998;
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                                                                                                                         regions from a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JANC ) JANSSEN PHARM NV
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reverse transcriptase; RNaseH; pseudol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon suppression; gene delivery; gene therapy vector;
390;
                   Similarity
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of Candida in a sample -
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98US-0106342
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                 6.1%;
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                                                                                       56 C;
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                                                                                                                           C. albicans strains
0;
Pred. No. 6.9
); Mismatches
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                                                                                       G; 128
               388.8; DB 1
No. 6.9e-70
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tgttggtttgtgcactattttgtgtcagaaactgatcaatgaaaatgatggttattatga

Gaps 60

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RESULT
AAA57931
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The invention relates to novel retrotransposons from the yeast Candida albicans which have a copy number of 40-150, preferably 50-100 copies per genome. In particular, the invention relates to the novel C. albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated form of this retrotransposon, designated TCa2, and to the novel C. albicans retrotransposons 1-28. pCal was initially isolated from C.
                                                                                                                               antigen, epitope or thera
presence of Candida in a
                                                                                                    Example 9;
                                                                                                                                            Novel retrotransposon expression vectors useful for expressing antigen, epitope or therapeutic agent, or detecting genes or the
                                                                                                                                                                                       WPI; 2000-365640/31.
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30-OCT-1998;
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reverse transcriptase; RNaseH; pseudoknot; readthrough translation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat;
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cic vaccine composition; immunogenic; transgenic
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98US-0106342
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                                                                                                 204pp;
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ARASULT
AAA5792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC abbicans hOG1042 and has a copy number of 50-100 copies per cell. It CC comprises identical 280 bp long terminal repeats (LTRs) and two open creading frames (ORFs). The first ORF encodes a gag (group antigen) CC protein, and the second ORF encodes a polyprotein (pol) consisting of an expartate protease, integrase, reverse transcriptase (RT) and RNaseH. The CC gag and pol ORFs of pCal are in the same reading frame, separated only by CC a termination codon (TGA). Translation of the pol ORF occurs through CC mediated by the formation of a pseudoknot within the gag-pol mRNA. CC The retrotransposons of the invention can be used as vectors for in CC vitro or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or CC immunogenic molecule (e.g., an antigen) and may also be used for CC eliciting an immunological response in a host organism. They are CC therefore useful in genetic vaccine compositions and for gene therapy, CC undesirable. Additionally, the retrotransposons may be used to generate CC transgenic animals, to detect the presence of Candida in a sample, to Generate and disrupt genes, and to assign functions to nucleotide corregions from a variety of C. albicans strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
         gag gene; group antigen; polyprotein; pol; asparate protease; integrase;
reverse transcriptase; RNaseH; pseudoknot; readthrough translation;
stop codon suppression; gene delivery; gene therapy vector;
                                                                                                                                                                                                                                                                   AAA57932 standard; DNA;
  genetic vaccine
                                                                                                                           Candida albicans strain F16-2 TCa2 retrotransposon 5' region.
                                                                                                                                                                                 10-OCT-2000
                                                                                 Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat; LTR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 392 BP; 136 A; 56 C; 72 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              361 gatagtttcggagtttgaaggtacagaatttc 392
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                                                                                                                                                                            (first entry)
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composition; immunogenic; transgenic animal; ds
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99.5%;
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Pred. No. 6.9e-70;
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Qy Вb QΥ Db Qy

181 tcaatatatatcttgtgaataataacttcgttctaattcactatacacaactagacgtgt

121 ataaataagggtatgaaataccaacatcccagaatatcaacgagatagaagggaggagtt

gaatggaaaatttttccatcacatcaggtgatgacagaactaaactatattgtgtagt gaatggaaaatttttccatcacacatcaggtgatgacagaactaaactatattgtgtagt

0;

ataaataagggtatgaaataccaacatcccagaatatcaacgagatagaagagaggagtt

121

61 61

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밁
                                              QΥ
                                                                                                                                                                                                         The invention relates to novel retrotransposons from the yeast Candida Calbicans which have a copy number of 40-150, preferably 50-100 copies CC per genome. In particular, the invention relates to the novel C. CC albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated Cform of this retrotransposon, designated TCa2, and to the novel C. CC albicans retrotransposons 1-80. pCal was initially isolated from C. CC albicans hodil42 and has a copy number of 50-100 copies per cell. It comprises identical 280 bp long terminal repeats (LTRs) and two open C. Creading frames (ORFs). The first ORF encodes a gag (group antigen) CC protein, and the second ORF encodes a polyprotein (pol) consisting of an appartate protease, integrase, reverse transcriptase (RT) and RNaseH. The gag and pol ORFs of pCal are in the same reading frame, separated only by a termination codon (TGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is certain the same reading frame separated only by the occasional readthrough suppression of the stop codon, which is certain the delivery and expression of the stop codon, which is certain the delivery and expression of the stop codon, which is certain the delivery and expression of a therapeutic, immunological or immunogenic molecule (e.g., an antigen) and may also be used for celiciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retroviral vectors is unsafe to generate transgenic animals, to detect the presence of Candida in a sample, to generate candidations to nucleotide.

Cc sequences. Sequences AAA57936 represents TCa2 retrotransposon 5' and in a variety of C albican strains.
                                                                                             Matches
                                                                                                                Best Local Similarity
                                                                                                                                                                                                       Sequence 392 BP; 136 A; 56 C; 72 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Fig 9; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel retrotransposon expression vectors useful for expressing an antigen, epitope or therapeutic agent, or detecting genes or the presence of Candida in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365640/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-OCT-1998;
30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999;
                                                                                                                                                                                                                                                 regions from a variety of C. albicans strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200026397-A1
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         \vdash
tgttggtttgtgcactattttgtgtcagaaactgatcaatgaaaatgatggttattatga
                                                                                           Conservative
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                                                                                                              6.1%;
                                                                                           0;
                                                                                    Score 388.8; DB Z1;
Pred. No. 6.9e-70;
Pred. No. 6.9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelissen BJM,
                                                                                                                                DB 21; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poulter RTM:
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                                                                                      Gaps
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RESULT
AAA57925
                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel retrotransposons from the yeast Candida albicans which have a copy number of 40-150, preferably 50-100 copies per genome. In particular, the invention relates to the novel C. albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated form of this retrotransposon, designated Tca2, and to the novel C. albicans retrotransposons 1-28, pCal was initially isolated from C. albicans hGG1042 and has a copy number of 50-100 copies per cell. It
                                                                                                                                                            comprises identical 280 bp long terminal repeats (LTRs) and two open reading frames (ORFs). The first ORF encodes a gag (group antigen) protein, and the second ORF encodes a polyprotein (pol) consisting of an aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The gag and pol ORFs of pCal are in the same reading frame, separated only by a termination codon (TGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is
                               mediated by the formation of a pseudoknot within the gag-pol mRNA. The retrotransposons of the invention can be used as vectors for in vito transformation and expression. Set as vectors thus be used for the delivery and expression of a therapeutic, immunological or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel retrotransposon expression vectors useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Fig 9; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence of Candida in a sample
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luyten WHML,
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30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic
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      immunogenic molecule
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98US-0106342.
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(e.g., an antigen) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nelissen BJM,
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   may also be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate transgenic animals, to detect the presence of Candida in a sample, to
                                                          30-OCT-1998;
30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                               Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                   stop codon suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans strain SA4-1 TCa2 retrotransposon 5' region.
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reverse transcriptase; RNaseH; pseudoknot; readthrough translation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat; LTR;
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98US-0106342.
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                                                                                                                                                                                                                                                                                                                                                                                                         immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                   delivery; gene therapy vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
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aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The care and pol ORFs of pCal are in the same reading frame, separated only by a termination codon (TGA). Translation of the pol ORFs occurs through the occasional readthrough suppression of the stop codon, which is mediated by the formation of a pseudoknot within the gag-pol mRNA. The retrotransposons of the invention can be used as vectors for in convitro or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or immunogenic molecule (e.g., an antigen) and may also be used for immunogenic molecule (e.g., an antigen) and may also be used for therefore useful in genetic vaccine compositions and for gene therapy, therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate thransgenic animals, to detect the presence of candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide compositions from a variety of C. albicans strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel retrotransposons from the yeast Candida albicans which have a copy number of 40-150, preferably 50-100 copies per genome. In particular, the invention relates to the novel C. albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated form of this retrotransposon, designated TCa2, and to the novel C. albicans retrotransposons 1-28. pCal was initially isolated from C. albicans hOG1042 and has a copy number of 50-100 copies per cell. It comprises identical 280 bp long terminal repeats (ITMS) and two open reading frames (ORFs). The first ORF encodes a gag (group antigen) protein, and the second ORF encodes a polyprotein (pD1) consisting of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel retrotransposon expression vectors useful for expressing an antigen, epitope or therapeutic agent, or detecting genes or the presence of Candida in a sample - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelissen BJM, Poulter RTM;
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Matches Query Match Best Local Similarity 389; Conservative 6.0%; 0; Score 387.2; Pred. No. 1. Mismatches 1.5e-69; DB 21; Length 392; Indels 0; Gaps 0,

Sequence

392 BP;

135 A;

57

c;

72 G; 128 T; 0 other;

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gatagtttcgaagtttgaaggtacagaatttc 392
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                                             aatcatttcgtcccaaattagcgttgtataaattcagtcctcagatttgtattattgatt
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AAA57933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans strain 759-1.
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                                                                                                                                                                                                                                                                        Example 9; Fig 9; 204pp; English.
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                                                                                                                                                                                                                                                                                                                                                                (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1998;
30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic vaccine composition;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                               De Backer MD,
                                                                                                                                                                                                                                                                                                                                                                                  98CA-2249046.
98US-0106342.
                                                                                                                                                                                                                                                                                                                                                                                                            99WO-NZ00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain 759-1 TCa2 retrotransposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenic; transgenic animal; ds
                                                                                                                                                                                                                                                                                                                                               Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                               Poulter RTM;
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The invention relates to novel retrotransposons from the yeast Candida CC albicans which have a copy number of 40-150, preferably 50-100 copies CC per genome. In particular, the invention relates to the novel C. CC albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated Cform of this retrotransposon, designated TCa2, and to the novel C. CC albicans hOG1042 and has a copy number of 50-100 copies per cell. It CC comprises identical 280 bp long terminal repeats (LTPs) and two open CC reading frames (ORFs). The first ORF encodes a gag (group antigen) CC protein, and the second ORF encodes a polyprotein (pol) consisting of an CC aspartate protease, integrase, reverse transcriptase (RT) and RMSASH. The GC gag and pol ORFs of pCal are in the same reading frame, separated only by a termination codon (TGA). Translation of the pol ORF occurs through CC the occasional readthrough suppression of the stop codon, which is CC mediated by the formation and expression. They can thus be used CC vitto or in vivo transformation and expression. They can thus be used for immunogenic molecule (e.g., an antigen) and may also be used for CC eliciting an immunological response in a host organism. They are CC undesirable. Additionally, the retrotransposons may be used to generate CC undesirable. Additionally, the retrotransposons may be used to generate transgenic animals, to detect the presence of Candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide sequences. Sequences AAA57923-A57936 represents TCa2 retrotransposon regions from a variety of C. albicans strains.

Sequence 392 BP; 138 Α; 57 C; 71 G; 126 T; 0 other;

밁

gatagtttcggagtttgaaggtacagaatttc 392

Matches

Conservative

99.28;

Best Local Similarity

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AAA57930
ID AAA57
AC AAA5
AC AAA5
XX AAA5
XX AAA5
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The invention relates to novel retrotransposons from the yeast albicans which have a copy number of 40-150, preferably 50-100
                                                                       Novel retrotransposon expression vectors useful for antigen, epitope or therapeutic agent, or detecting presence of Candida in a sample - \,
                                                                                                                                                                                                                      30-OCT-1998;
30-OCT-1998;
                                              Example 9; Fig
                                                                                                                                                             Luyten WHML,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Retrotransposon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans strain SA4-2 TCa2 retrotransposon 5' region.
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                                                                                                                                                              De Backer MD,
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98US-0106342.
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                                                                                                                                                                                                                                                                                                                                                                                 composition; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                         pCal; TCa2; Tyl; copia; long terminal repeat; LTR;
                                                                                                                                                                                                                                                                                                                                                     strain SA4-2
                                              204pp; English.
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                                                                                                                                                             Nelissen BJM,
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                                                                                                                                                                                                                                                                                                                                                                                 transgenic animal; ds
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copies

10-OCT-2000

(first entry)

Candida albicans strain 759-2 TCa2 retrotransposon 5' region.

pCal; TCa2; Ty1; copia; long

repeat;

AAA57934

AAA57934 standard;

DNA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 392 BP; 135 A; 58 C; 72 G; 127 T; 0 other;
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                                        gatagtttcgaagtttgaaggtacagaatttc 392
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Pred. No. 3.
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CC form of this retrotransposon, designated TGA, and to the novel C. C. albicans retrotransposons 1-28. pCal was initially isolated from C. C. albicans hog1042 and has a copy number of 50-100 copies per cell. It C. comprises identical 280 bp long terminal repeats (LTRs) and two open C. C. reading frames (ORFs). The first ORF encodes a gag (group antigen) C. C. protein, and the second ORF encodes a polyprotein (pol) consisting of an C. aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The G. C. gag and pol ORFs of pCal are in the same reading frame, separated only by the cocasional readthrough suppression of the stop codon, which is C. C. The retrotransposons of the invention can be used as vectors for in C. C. The retrotransposons of the invention can be used as vectors for in C. C. The delivery and expression of a therapeutic, immunological or immunological response in a host organism. They are considered in genetic vaccine compositions and for gene therapy, C. C. c. c. and disrupt genes, and to assign functions to nucleotide transgenic animals, to detect the presence of Candida in a sample, to C. G. c. albicans strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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(JANC ) JANSSEN PHARM NV.
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387; Conserv
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98US-0106342.
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Pred. No. 6.
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5.5e-69;
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CC The invention relates to novel retrotransposons from the yeast Candida CC albicans which have a copy number of 40-150, preferably 50-100 copies CC per genome. In particular, the invention relates to the novel C. CC albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated CC, form of this retrotransposon, designated TCa2, and to the novel C. CC albicans retrotransposons 1-28. pCal was initially isolated from C. CC calbicans hOG1042 and has a copy number of 50-100 copies per cell. It CC comprises identical 280 bp long terminal repeats (LTRs) and two open CC reading frames (OREs). The first ORF encodes a gag (group antigen) CC protein, and the second ORF encodes a polyprotein (pDl) consisting of an CC aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The CC gag and pol ORFs of pCal are in the same reading frame, separated only by CC a termination codon (TGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is compared to the formation of a pseudoknot within the gag-pol mRNA.
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presence of Candida in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stop codon suppression; gene delivery; gene therapy vector; genetic vaccine composition; immunogenic; transgenic animal
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                                                                                                                                                                                                                     Retrotransposon; pCal; TCa2; Ty1; copia; long terminal repeat; LTR; gag gene; group antigen; polyprotein; pol; asparate protease; integreverse transcriptase; RNaseH; pseudoknot; readthrough translation;
                01-NOV-1999;
                                                             11-MAY-2000
                                                                                                   WO200026397-A1
                                                                                                                                           Candida albicans
                                                                                                                                                                                 genetic vaccine
                                                                                                                                                                                                                                                                                                        Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAA57924 standard; DNA; 392
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                                                                                                                                                                                                    codon suppression; gene delivery; gene therapy vector;
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87; Conservative
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                     99WO-NZ00179
                                                                                                                                                                                   composition; immunogenic;
                                                                                                                                                                                                                                                                                                        strain SGY-2 TCa2 retrotransposon 5' region
                                                                                                                                           strain SGY-2
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98.7%;
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Pred. No. 6.5e-69;
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                                                                                                                                                                                   transgenic animal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aspartate protesse, integrase, reverse transcriptase (RT) and RNAseH. Thy gag and pol ORFs of pCal are in the same reading frame, separated only k a termination codon (YGA). Translation of the pol ORF occurs through the occasional readthrough suppression of the stop codon, which is mediated by the formation of a pseudoknot within the gag-pol mRNA. The retrotransposons of the invention can be used as vectors for in vitro or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or immunogenic molecule (e.g., an antigen) and may also be used for eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate transgrand animals to Advant the procession of a contract transgrand animals to Advant the procession of a contract transgrand animals to Advant the procession of a contract transgrand animals to Advant the procession of a contract transgrand animals to Advant the procession of the stop transgrand animals to Advant the procession of the stop transgrand animals to Advant the procession of the stop the procession of the stop transgrand animals to Advant the procession of the stop transgrand to generate transgrand animals to Advant the procession of the procession of the stop transgrand to generate transgrand animals to Advant the procession of the stop transgrand to generate transgrand animals to Advant the procession of the stop transgrand to generate transgrand animals to Advant the procession of the stop transgrand to generate transgrand animals to Advant the procession of the stop transgrand to generate transgrand transgrand transgrand transgrand transgran
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30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic animals, to detect the presence of Candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide sequences. Sequences AAA57923-A57936 represents TCa2 retrotransposon 5' regions from a variety of C. albicans strains.
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acacgctcaatctcaggtaaagaaagtttatattccatcagattagaagtcaaaagcgat
                            acacgctcaatctcaggtaaagaaagtttatatttccatcagattagaagtcgatagtgat 300
                                                                                                                       tcaatatatatcttgtgaataataacttcgttctaattcactatacacaactaggcgtgt 240
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98US-0106342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 382.4; DB 2
Pred. No. 1.4e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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genes or the
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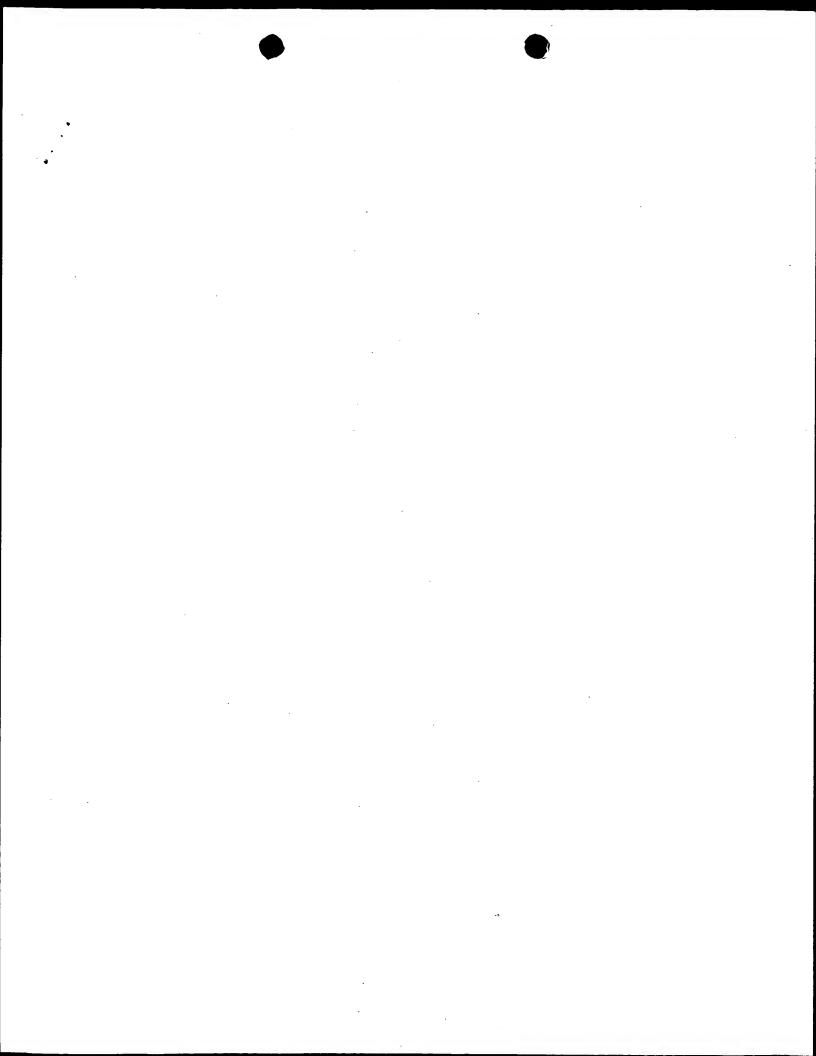
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel retrotransposons from the yeast Candida CC albicans which have a copy number of 40-150, preferably 50-100 copies CC per genome. In particular, the invention relates to the novel C. CC albicans Tyl/copia retrotransposon pCal (AAA57920), and to the integrated CC form of this retrotransposon, designated TCa2, and to the novel C. CC albicans retrotransposons 1-28. pCal was initially isolated from C. CC albicans hOG1042 and has a copy number of 50-100 copies.per cell. It CC comprises identical 280 bp long terminal repeats (LTRs) and two open CC reading frames (ORFS). The first ORF encodes a gag (group antigen) CC protein, and the second ORF encodes a polyprotein (pol) consisting of an CC aspartate protease, integrase, reverse transcriptase (RT) and RNaseH. The CC gag and pol ORFs of pCal are in the same reading frame, separated only by CC a termination codon (TGA). Translation of the pol ORF occurs through CC mediated by the formation of a pseudoknot within the gag-pol mRNA.
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                                                                                                                                                                          The retrotransposons of the invention can be used as vectors for in vitro or in vivo transformation and expression. They can thus be used for the delivery and expression of a therapeutic, immunological or immunological or antigen) and may also be used for eliciting an immunological response in a host organism. They are therefore useful in genetic vaccine compositions and for gene therapy, particularly where the use of retroviral vectors is unsafe or undesirable. Additionally, the retrotransposons may be used to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel retrotransposon expression vectors useful for expressing an antigen, epitope or therapeutic agent, or detecting genes or the presence of Candida in a sample -
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                                                                   transgenic animals, to detect the presence of Candida in a sample, to detect and disrupt genes, and to assign functions to nucleotide sequences. Sequences AAA57923-A57936 represents TCa2 retrotransposon 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Fig 9; 204pp; English.
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30-OCT-1998;
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                                       regions from a variety of C. albicans strains.
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Search completed: August 25, 2001, 02:35:04 Job time: 13259 sec



Run on:

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Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACCESSION
VERSION
KEYWORDS
  COMMENT
                                REFERENCE
                                                            SOURCE
                                                                                                 DEFINITION
                                                                                                               AI813079
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         JOURNAL
                 TITLE
                                                     ORGANISM
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       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 569)
Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Unpublished (1999)
Contact: Ross Whetten
                                                      Pinus taeda
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     ENTEV58TR Entamoeba
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North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh, NC, 27695-8008
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primer: T3.
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/clone_lib="Pine Lambda Zap Xylem library"
/clone_rib="Pine Lambda Zap Xylem"
/tissue_type="differentiating xylem"
/note="Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI;
Differentiating xylem was collected from the main stem
a 35-year old loblolly pine tree harvested during the
growing season. RNA isolation and library preparation
followed the methods of Allona et al., PNAS 95:9693-8,
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Brendan J Loftus
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."

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Pred. No. 8.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/db_xref="taxon:7227"
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Best Local Similarity 17.3 Matches 118; Conservative

289;

Mismatches

274;

Indels Length 1101;

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Gaps

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Query Match

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REFERENCE
AUTHORS
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AZ546009/c
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                                                                                                                                                                                                             TITLE
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                     Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTWTWTTWWAATTATTTTWT 420
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Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                              Entamoeba histolytica.
Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                           AZ546009.1 GI:11167130 GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                             genomic, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ546009
                                                                                                                                                                                                                                                   (bases 1 to 849)
bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                   849 bp
                                                                  MD 20850, USA
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                              4079 gaatttgaaacgtataatgttgatgaaattgagaatgtgattaatgacgatgacattgct 4138
                                                                                                                 4019 aaaaatactgaaataatccaaaaaacacattgaaagtatccttgctgataagagattggat 4078
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517
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Local Similarity 46.7%;
                                                                                                                                                                                                                                                                                                                                                  atacttaatgaacaaactgatatagttgatactgttgctaaagttattgagaatgaaaaa 3898
                                                                                 agcaattcaacagaatccgacattcaatcgaaaaatgaaatatcaccagtgattaatgag 4018
                                                                                                                                                                                                                                             gttgaaacagaggatgctggtaacagtccaattcaagacgaagtttctcaagagggaaga 3838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atctctcctattaattcattagatgatcatactgaacttgctacagactcgggaaatgat 3958
                                                                                                                                                                                                                                                                                                                             GAAGATGATGATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                            ccctcgttactggctaataagaatcgggtaactgaaaaaatagatgagggagaaaatatt 3718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 26
High quality sequence stop: 796
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotun sequencing projects In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Entamoeba histolytica"
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TITLE
JOURNAL
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les 212; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPG1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://baccac.med.buffalo.edu/drosophila bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gaagctaatccactaccagatgaaaataatgatgtt 4174
|||| || || || || || || || 6
GAAGATGATGAAGATGATGAAGATGACGAAGAT 65
ttgcagcaaaaccacgtttccagtagaaaattctcattctctttaatgcttctttgaacgt 1476
                                                                                                                                                                                                                                                        aaataagaaacatccaaaatcagataacgataaaggtgaaaaagaaaaagaaaaagaaaa 1356
                                                                                                                                                                                                                                                                                                                CNSOOLT2 1101 bp DNA GSS 14-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Location/Qualifiers
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/clone="BACR48P19"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                             El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sul
Gerrard, C., Leech, V., de Jong, P., Ullu, E.,
Fraser, C. and Adams, M.
                                                                                                                                                                                                                                         Tel:
                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_GSSs: Sheared DNA-46J23.TF
                                                                                                http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
                                                                                                                                     Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page:
                                                                                                                                                                                                                                                                                                                   Contact: Najib M. El-Sayed
                                                                                                                                                                                                                                                                                                                                                                          Determination of clone end sequences from Trypanosoma brucei GUTat 10.1\ \mathrm{sheared}\ \mathrm{DNA}\ \mathrm{library}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                Email: nelsayed@tigr.org
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                                                                                                                                                                                                                     301 838 0200
301 838 0208
                                                                                  shotgun.
/organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
                                                         ocation/Qualifiers
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                      254;
                                                                   GSS.
                                                                                                                                         AZ531291 877 bp DNA GSS 03-NOV-2000 ENTBQ34TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
                   Entamoeba histolytica.
Entamoeba histolytica
                                                                                                        genomic, DNA sequence. AZ531291
  Eukaryota;
                                                                                    AZ531291.1
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/clone_lib="Sheared DNA"
/note="vector: pUC18; Site_l: Smal; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barell, Oxford University
Press, 1999)."
                                                                                    GI:11085838
Entamoebidae; Entamoeba
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                              3899 atctctcctattaattcattagatgatcatactgaacttgctacagactcgggaaatgat 3958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
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Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1: LMSS, sheared DNA library
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The Institute for Genomic Research
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/note="Vector: pHOS1; Site_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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/db_xref="taxon:5759"
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Pred. No. 9.5e-07;
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A BAC End Sequencing Framework to Sequence the
Unpublished (1998)
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100 Jordan Hall, Clemson,
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Class: BAC ends
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/note="vector: pBACIndigo; Site_1: ECORI; Site_2: ECORI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mpp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Nipponbare"
/db_xref="taxon:4530"
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High quality sequence stop: 235
Location/Qualifiers
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                                                                                                                     Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                             Clemson University
100 Jordan Hall, C
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                                                                                                                                                                                                                           Contact: Wing RA
                                                                                                                                                                                                                                            Unpublished (1998)
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Similarity 52.8%;
                                                             Class:
                                                                            Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
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                                                                                                                                                             Clemson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AGGAAGCTGTTCCAGCCTTGCTTCGGGATTTACAAAAGGAGTTTGCTCTGAAGGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GAGATTTGATTATATTTGTACTCATTTATGTTGATGATATTATTGTCACCAGTTCTAGAC 183
                                                                                                                                                                                                                         424 CAAATGATGCAACACATTATAGAAGTGT 451
                                                                                                                                                                                                                                                                                                                                                   364 TTAGTACACCCCTGTCTACAAGTGAGAAATTGGCTATAAATGAAGGAGATCCTTTAAGAC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 CTCAAGATAAATATGTCAATGATTTGTTGAGAAGAGTNAATATGTTTGACTGCAAACCGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 GAGATCTTCATTACTTTCTTGGTATTGAGGTAACTAAAGTGTCTGGTGGTATAGTTCTTA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CTTTATATGGCTTAAAGCAGGCACCTAGAGCTTGGTACTCTAGGCTTAGCAAGAAGTTAT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224;
                           AZ549980 900 br
ENTDD94TF Entamoeba
genomic, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18.432 clones (doubly spotted), represent the whole library for colony screening."

99 c 139 g 221 t 1 others
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/lab_host="E. coli DH10B"
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/clone_lib="CUGI Rice BAC Library"
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/db_xref="taxon:4530"
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/strain="Japonica"
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                                                             900 bp
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1.5e-06;
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3882 ttattgagaatgaaaaaatctctcctattaattcattagatgatcatactgaacttgcta 3941
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                                                                                                                                                                                                                3762 atgttgagcaatctaatgttgaaacagaggatgctggtaacagtccaattcaagacgaag 3821
                                                                                                                                                                                                                                                                                                                 3702 atgagggagaaaatatttcatttccggggggtgatgatgattctgtcgtgatcaactcaa 3761
                                                                                                                                                                                                                                                                                                                                                                                                          3642 aagatgaacagcaaaatccctcgttactggctaataagaatcgggtaactgaaaaaatag 3701
                                                                                                                     3822 tttctcaagagggaagaatacttaatgaacaaactgatatagttgatactgttgctaaag 3881
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                                                                         467 ATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGA
                                                                                                                                                                                                                                                                              347
                                                                                                                                                                                                                                                                                                                                                                  287 TAGATGACGAAGAATTTGACTTAGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 TTGAATTAGAAGAAGACTTTCAAAATGATAATGACTATGAATTAGAAAACAATGAAGATT 286
                                                                                                                                                                        AAGATGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGACGATG
                                                                                                                                                                                                                                                                   AAGATGAAGACGAAGACGATGAAGACGATGAAGATGATGAAGATGATGAAGATGATG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281;
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Tel: 301 838 0200
Fax: 301 838 0208
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AZ549980.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13-Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
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/Clone="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Score 77.8; DB 245; Pred. No. 2.8e-06;

Length 912;

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The Institute for Genomic Research
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Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Dr., Rockville, 301 838 0200
              /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
/note="Vector: pHOS1; Site_1: Rockville; MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450 ). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotuun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                   Drosophila melanogaster
                                                                                                                                                            fly), genomic survey sequence. ALO61936
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1713 ttgtgagtttgaaacaaattgaagaacgaggatttaatgttcttattactaaagaatcag 1772
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                              atctgttgtgaacaat----aaagatatattgctgaatgttaaggacgcaacaattgaag 1592
                                                 tcggtattgtctcgattacgttagagaatacattgtatttaccagaaagttcctttaatc 1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
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/db_xref="taxon:7227"
/clone_ilb="RPCI-98"
/clone="BACR05N11"
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39.3%; Pred. No. 2.9e-06;
ative 54; Mismatches 429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_llb="ToxoBAC"
/clone="BACNO8012"
/note="end: T7"
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GSS.
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100 Jordan Hall, C
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864 656 4293
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genomic information from. To facilitate the genome analysis of tomato, we have constructed a tomato BAC library that is suitable for positional cloning, physical mapping, and genome sequencing. The library contains 129,000 clones and a random sampling of 498 clones indicated an average insert size of 117.5 kb. With 15X haphoid genome equivalents (1C equals 953 Mb) (Arumuganathan and Earle, 1991), the probability to recover any particular sequence is greater than 998. High stability, large insert
                                                                                                                                                                                 /note="Vector: pBeloBAC 11; Site_1: HindIII; Site_2: HindIII; Tomato is a vegetable crop that ranks second only to potatoes in value and importance. Among plant geneticists and physiologists, tomato represents an ideal dicot model beside Arabidopsis and monocot rice to derive
                                                                                                                                                                                                                                                                                                                               /clone="toxb0001L16r"
/clone_lib="CUGI Tomato BAC Library"
                                                                                                                                                                                                                                                                                       /tissue_type="Nuclei preparation from Leaf"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Heinz 1706"
/db_xref="taxon:4081"
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AZ548467
          Unpublished (2000)
Contact: Brendan
                                                                                     Eukaryota; Entamoebidae; Entamoeba
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Loftus, B., Van Aken, S. and Fraser, C.
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dq 806

histolytica Sheared DNA Entamoeba histolytica

14-NOV-2000

J Loftus

from Entamoeba histolytica

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4668 gacaaaaggaaaaattggattatgacccttttagtgtttagttcacctgttatagatcttg 4727
                               5208 aatttotcaagaaattacttaaggattttcaaactagatgactc 5250
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AGTACATTAAGGAGCTACTGAAGAAATTCAATATGTTTGACTC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tomato BAC library, and preliminary analysis of the 1536 tomato BAC end sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                  aagagggaagaatacttaatgaacaaactgatatagttgatactgttgctaaagttattg 3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agcaatctaatgttgaaacagaggatgctggtaacagtccaattcaagacgaagtttctc 3827
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                                                                                tgattaatgagaaaaatactgaaataatccaaaaacacattgaaaagtatccttgctgata 4067
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High quality sequence stop: 828
Location/Qualifiers
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Seq primer: M13-Reverse
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Email: bjloftus@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolyti
using a method described by Clark and Diamond (Clark,
using a method described by Clark and Diamond (Clark,
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/strain="HM1:IMSS"
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Pred. No. 9.3e-06;
0; Mismatches 401;
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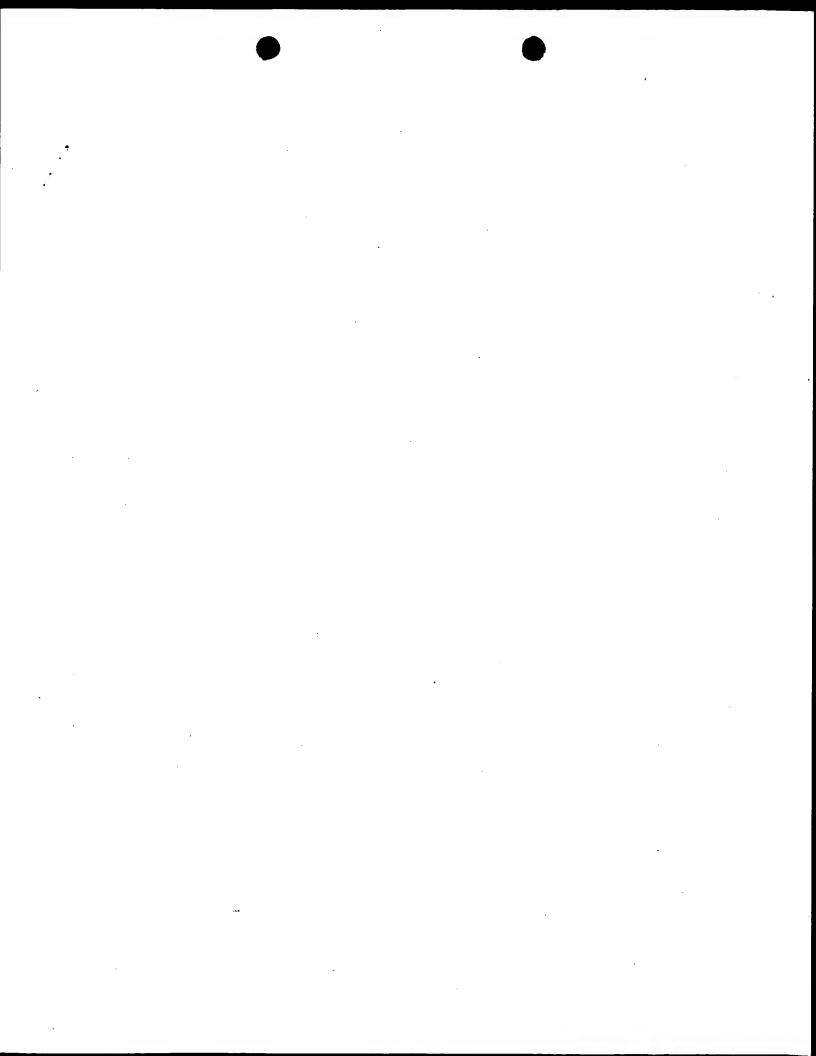
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Search completed: August 25, Job time: 6426 sec 2001, 00:08:01 FEATURES



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August 24, 2001, 22:49:15; Search time 8259.91 Seconds (without alignments) 12033.516 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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166 142.4	339.2 1 74 .6	400	432	6421.2	6426	Score
2.6	5.3 2.7	6.2	6.7	99.9	100.0	Query Match Length DB
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10 53	12 53	12	14	12	12	DB
AX073190 CNS07ACX	AF078809 CNS07BJD	AF030556	CAL251464	AF050215	AF007776	ID
AX073190 Sequence AL436423 T3 end of	AF078809 Candida a AL437951 T7 end of	AF030556 Candida a	AJ251464 Candida a	AF0502I5 Candida a	AF007776 Candida a	Description

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                                                                                                                         pCal, a highly unusual Tyl/copia retrotransposon from the pathogenic yeast Candida albicans
J. Bacteriol. 179 (22), 7118-7128 (1997)
                                                                                                                                                    Matthews,G.D., Goodwin,T.J., Butler,M.I., Berryman,T.A. and Poulter,R.T.
                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. 1 (bases 1 to 6426)
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Candida albicans
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                                                                                               Matthews, G.D., Goodwin, T.J.D., Butler, M.I.,
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                transposon="retrotransposon pCal"
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                                                            (11-JUN-1997) Department of Biochemistry, University of \kappa 56, Dunedin, New Zealand
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AC074284 Oryza sat
AC092867 Oryza sat
                                                                                                                                                                                                                                                                                                                                                                          AP002867 Oryza sat
AC091086 Oryza sat
AP002747 Oryza sat
AP002747 Oryza sat
AC006278 Plasmodiu
U72726 Oryza longi
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AP003311
U68072 Ly
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AL436847
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AJ005762 Phaseolus
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Y08010 A.thaliana
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AC079604 Arabidops
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T7 end of
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Best Local Similarity
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61 gaatggaaaatttttccatcacacatcaggtgatgacagaactaaactatattgtgtagt 120
                                                                                              1 tgttggtttgtgcactattttgtgtcagaaactgatcaatgaaaatgatggttattattga 60
                                                            TGTTGGTTTGTGCACTATTTTGTGTCAGAAACTGATCAATGAAAATGATGGTTATTATGA
                                                                                                                                                                                       Conservative
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6147. .6426
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QYEVRCTYVESEYDNTNDVMHHPKESYSYQPASFILTIGNSSREYVINDDPVQITIEN
PDDFSNPLQLTEESHDMYSEVKSDENDRYSLHELTFGDNPVSKEPQLGTETSYIGKSK
EPITNHTKDAPSIQGRDHKRSESTAQVGLSHQPQTGTPASEESKLSGTDHFGVDVVKE
TVSEDMHTSDYEPTSAEDEQQMPSLSAHKNRVTEKIDEGENLSFPGGDDSVVINSNV
EQSNVETEDAGNSPIQDEVQDERILLNEQTDIVTDVAKVIENDRYLLN
EQSNVETEDAGNSPIQDEVQDERILLNEQTDIVTDVAKVIENDRYLLN
TDSGNISNTESDIQSKNEISPYINEKNTEIIQKHIESILADKRLDEFTYNVDEIEN
VINDDIELANNFLPDENNDQMNESFDNNHSMSRAKKKYFFKEVNEKIAFTHSLDT
TDSGNISNTESDIQSKNEISPYINEKNTEIIQKDEVAKKKYFFKEVNEKIAFTHSLDT
TDSGNISNTESDIQSKNEISPYINEKNTEIIQKDEVAKKKYFFKEVNEKIAFTHSLDT
TDSGNISNTESDIQSKNEISPYINEKNTEIIQKDEVAKKKYFFKEVNEKIAFTHSLDT
TDSGNISNTESDIQSKNEISPYINEKNTEIIQKDEVAKKKYFFKEVNEKIAFTHSLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Region: polypurine tract 2"
6136. .6146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDPREAIRVLNTGETKRIEPKKREVPITVKLNKRSQYKSPYVTRSGRTVINPKRYLHA
VVNKLIDYNDEGWIKSMABELEKFRSKDYYEEVPIPTGYVFIJENGWYHTEKIDSLKGVV
RKSRCVYHGHRAKOKEKLDYDPFSVSSFYJIDLYT FLLT IIGELGMT1QHLDVESAYLN
ASITHSNPIYVFPKSVPLKKNHCWLLKRSVYGLKQSGLEWYHTIKRVLEDIGFTQVL
HNDGLFHIEYEEGSVIYLGLEYVDDILMVGSSQKVIDNFVDQLADHFEVKVFGEISNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSEESLECDFDYDGLADMLSNANQDDKDKSSMNEMSEYQEHDYSSRALINSLTEVDVL
DVEISPYGVEQLLPTGDKNDIYNFHLMSNHMSIEKILLLQKYQGLVLHTSKESLQKIA
DCKVCLLSNAKQRSHNHHSERKASRRHERLHCDTLGPFRSENNKWYLTSVIDEHTGYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Region: 3455. .3465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Region: purine-rich tract"
1381. .1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIEFRKTESGY ILSQEKFLKKLLKDFKLDDSYGKNIPWIPNDKYEKVAII RENVNPEN
DFEKVPNETLLDPDAKKLYQSGVGSLLWAATNTRPDISVVVNSLGSKSANPNVHDYEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGIITKDRKVKDLLIQRLKIWNNRFNDKVAYFRSDNAPEFPQPSDLAEFGIWRETIAA
YSPELNGLAEVVNKLILQQIYRIVVTLGPQILKLIYYVIQYSITMINHTPRRSLKGQT
PYGCYYQLSEGNFYRFPFAIDCVVTFSNAIEKNRYGVTSTKGAPSSIMGAVIGYASDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation~"KTGAASINCVMNIHNCSKTTFPVENSHSLNASLNVMNFKGLRFN
KYLVYDTGATISVVNNKDILSNVKDATIEVSVADGATLEADCIGDLIIRVGIVSITLE
NTLYLPESSFNLVSLKQIEERGFNVLITKESVIVFNQNVAPTIIASRKNAADLYMGPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="POL protein"
/protein_id="AAC49878.1"
/db_xref="GI:2636719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="potentially suppressed stop codon" <1373. .6103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVCYNLPYLSQVEEKLEETLYNTSNVVDEYVRSLPNLIGQVLYFNHVKKSEALSLFLN
THASYYSKWIQADNDTSVLPSCSTIAEEMCDHPDYARLVDIPSNKYELNLIVSLPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKLAVGNQKSVDKWNEEFKYFHVAYPDVLEFLLDYNPKDKFKVKKVEGIYFTGWCLQM
CLQSIFDRFRLIMISKLPKHLQKEANLIKAAYDAVTKSKDYTITSKILSKFVNVEHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Minus-strand primer-binding site" 398. .1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGMIKRLDLEDNQTSIQNAITAE"
1373. .1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLVQWATKKQTVIAQSSAACEMLALNYTMLKAIEIKNHLMDLGFEVGKIHCHQDNQAV
IKVLRNNYCHPHRPIDICYKFLRQLINDKVFSISYVKTNDNYADCMTKCLSRAKFKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIYCLRYIKNSMGYHIEYKRNRLNIPPKSFYIECFSDASFAPGLDRKSISGTLIYVNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPKGKPEENSSEQSQKKNSKSRKRNKKHPKSDNDKGEKEKEKEKTSSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="GAG protein"
/protein_1d="AAC49879; 1"
/db_xref="G1:2636720"
/translation="MSSAKNDDNEGKVMESVDQANAISKVDEHIKARFNMLFIKFNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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1031 c
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                                                                                                                                                                                                                                                                                                                                                                    1259 g
                                                                                                                                                                                    Score 6426;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potential pseudoknot"
                                                                                                                                                                                                                                                   DB
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                                                                                                                                                                                    'Indels
                                                                                                                                                                                                                                            Length 6426;
                                                                                                                                                                                    0;
                                                                                                                                                                                Gaps
                                                               60
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dd Db	1200	41 tgatcatcctgattatgctagattggttgacattccaagcaacaaatatgaacttaatct	Qy 11
מם	1140	81 tcaagctgacaatgatacatcagtactcccaagttgctctaccatagctgaagaaatgtg	Qy 10
	1140		Db 10
da	1080	21 gaaatcagaggctttaagtttgtttttgaatattcatgcctcatactactcaaagtggat	Qy 10
da			Db 10
- D	1020	61 tgagtatgtccgtagtcttccaaatctcataggtcaagtcttgtacttcaatcatgtgaa	Qy 9
	1020		Db 9
מם מס	960	01 tttgctgcaggtggaagagaaacttgaggaaatactctacaacacttcaaacgttgtcga 	Qy 9
ם מ	900	141 gatottgotgaagtttgtaaacgttgaacatgagttagtggtttgctataaccttccata 	Qy 8
Db C:	8 4 0	81 cttaatcaaagctgcttatgatgctgttactaaatctaaagattataccattactagtaa	Qy 7
	840		Db 7
Db Cr	780 780	21 tgataggttcagattgatcatgatttctaagctaccaaagcacttgcaaaaggaagcaaa	Qy 7 Db 7
מם מס	720 720	61 aaaggtagaaggtatttattttactggttggtgtttacaaatgtgtttacagtccattt	Ωy 6 Db 6
מ ט	660	01 ttaccccgatgtttttggaatttttgcttgactataatcctaaagataaattcaaggttaa 	Qy 6
מם מס	600	41 cgtcggtaatcagaaaagcgtggataaatggaatgaagaatttaaatatttccacgttgc 	Qy 5
מם	540	81 acatatcaaggctagattcaatatgcttttcataaaatttaatgacttacctaagttggc	Qy 4
	540		Db 4
מס סט	480	21 taacgaagggaaggtcatggaaagtgttgatcaagctaatgctattagtaaggtggatga	Qy 4
	480	-	Db 4
מם מס	420	861 gatagtttogaagtttgaaggtacagaatttcacaagatgagttccgcaaagaatgatga	Qy 3
	420		Db 3
4d 4d 4d	360	301 aatcatttegteccaaattagegttgtataaattcagtecteagatttgtattattgatt	Qу 3
	360		Db 3
Db Qy	300	241 acacgeteaateteaggtaaagaaagtttatatteeateagattagaagtegatagtgat 	Qy 2 Db 2
da	240	181 tcaatatatcttgtgaataataacttcgttctaattcactatacacaactagacgtgt	Qу 1
Vy	240		Db 1
QQ QQ	180	121 ataaataagggtatgaaataccaacatcccagaatatcaacgagatagaagggaggtt	Qy 1
	180		Db 1
da da	120		Db

.aagcctcgagaagaca 2280 AAGCCTCGAGAAGACA 2280	atogaatgccaaacagagaagtcacaatcatcattcagaaagaa	2221 2221	Qy Db
gtaaggtatgtctatt 2220 	cgtacttcacacttcaaaagagagtcttcaaaagattgctgattc 	1 1	Qy Db
aaaaataccagggtct 2160 	tttgatgtcaaatcatatgtccattgagaaaatcttgttgttacs	10	Qy Db
atatttataatttcca 2100 	:ccatatggagttgaacaattgctaccaactggagataagaacg 	0 0	Оy
tagatgttgaaatttc 2040 TAGATGTTGAAATTTC 2040	tagttctcgagcattaataaattctttgacggaggttgatgttt	96	Qу
atcaagaacatgatta 1980 ATCAAGAACATGATTA 1980	Caagatgacaaagataaatcaagtatgaatgaaatgtcagaat 	92 92	Qy Db
ttgttgtccaatgctaa 1920 	agaatctttagaatgtgattttgattatgatggtttggcagatat 	ထ ထ	Оy
gtcctcaattcagtga GTCCTCAATTCAGTGA	tactattattgcttcaaggaagaatgctgctgatctttatatgg	ထ ထ	Qy Db
AACCAAAATGTGGCTCC 1800	aggatttaatgttcttattactaaagaatcagtgattgtatttac 	1741 1741	Qу
aaacaaattgaagaacg 1740 NAACAAATTGAAGAACG 1740	tacattgtatttaccagaaagttcctttaatcttgtgagtttga:	1681 1681	ФФ
cgattacgttagagaa 1 CGATTACGTTAGAGAA 1	agcagattgtattggtgatctaattatcagagtcggtattgtct	1621 1621	Qy Db
atggtgctacattaga 1 	. attgctgaatgttaaggacgcaacaattgaagtttctgttgctg: 	UI UI	da Qy
tgaacaataaagatat TGAACAATAAAGATAT	acaagtatctagtgtatgatactggtgccacaatatctgttg 	ப் ப	дь Оу
ttaaaggtttaaggtt 15 TTAAAGGTTTAAGGTT 15	agaaaattotoattotottaatgottotttgaaogtaatgaatt	4 4	Qy Db
AAAACCACGTTTCCAGT 1440	tgctgcttctattaattgtgtaatgaatatacataattgcagca	1381 1381	Qу Db
otggaatgaaaaacagg 1380 	aaaacttcac AAAACTTCAC		Qy Db
naacatccaaaatcaga 1320 	. acaatotoaaaagaagaacotgaaatcaagaaagagaaagagaataaga; 	1261 1261	QУ
yaggagaactcactgga 1260 	tattgttagtttaccagcaccagagaaaccaaaaggaaaaccag 		Qy Db
AAATATGAACTTAATCT 1200	TGATCATCCTGATTATGCTAGATTGGTTGACATTCCAAGCAACA	1141	DЬ

3360 3360	cgaagtaaaatcggatgagaatcctaaacccagtctccacgagctaacacctggggataa	у 330 ъ 330	0 0
	aatcocgatgatttttctaaccctcttcaactaactgaagaatcacacgatatggtatc 	24	o o
	tacgggtaacagttctaacgaatatgttataaatgatgatccagtacagattaccattga 	y 318 b 318	o o
3180 3180	tgacgtgatgcacatgcccaaagagtcatattcagttcagccagc	N) N)	9 0
3120 3120	actgggcgctcagtacgaggtacgcggaacatatgtggaaagtgaatatgacaatacaaa 	306	g Qy
3060 3060	cttatccactacacctatgtcacacattgttcctatggctgaaggtatccagggaaggca 	3001 5 3001	
3000 3000	CCTTAGCCCTAATGTCCGTATATTGCGAAGCTATGAGGTTATTAACTCCTATCTCAAAAA	у 294 b 294	0 0
2940 2940	ctacgctagcgattgttttagttattacgtgtttgctaaaaaatatgcggtgtgatattat 	y 288 b 288	0 0
2880 2880	ccgttacggagttacatcaactaaaggagctccttcatcgatcatgggtgctgtgattgg 	y 282 b 282	
2820 2820	ctaccggtttccttttgccatcgattgtgtcgttacatttagtaatgccatcgaaaagaa 	y 276 b 276	0 10
2760 2760	tcgttcactcaagggacaaaccccttatggttgctattatcaattaagtgagggaaattt 	y 270 b 270	8
2700 2700	actcaagttgatttattatgtgattcaatattctattacaatgatcaaccacactccacg	264	문양
2640 2640	tgttaataaattgattttacaacagatttacaggatcgttgtgacacttggtccacaaat	2581 b 2581	2
2580 2580	cggtatttggagggagactatagcggcatatctgcctgagcttaatggtctcgccgaggt	252 252	, B 5
2520 2520	ggcatacttcagaagtgataatgctcctgagttcccacaaccttctgatttagctgagtt	246 246	8 8
2460 2460	ggtaaaggatctcttaattcaacgattaaagatctggaataatcggtttaacgataaggt	240	8 8
2400 2400	aacgtctgttatagatgaacatacgggttacattgaaggaattattactaaagacagaaa . 	234	8 8
2340 2340	tgagagacttcattgtgatactctcggtccatttaggtccgaaaataacaagtggtattt		9 .9

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AACAAAAGATCGCAATACAAGTCACCATATGTTACAAGAAGTGGTAGAACGGTTATAAA cccaagaggtatttacatgcggtcgtcaacaagatcgagctataatgatccggggatggat	aaacaaaayatcycaatacaaytcaccatatyttacaayaaytyytayaacyyttataaa	H —	actggtgaaaccaagagaatcgaacccaagaaaagagaggtgcctatcactgtgaaatt	> —	gctggtactaaacattcacttgatacaactgatccaagagaagcaatcagagtgttaaa	⊣ ⊢	catagcatgtcacgagcaaagaagaaatacacatttgagaaagaa	CTAATCCACTACCAGATGAAAATAATGATGTTCAGATGAGAGGTTTTGATAATAA	gctaatccactaccagatgaaaataatgatgttcagatgaatga	TTTGAAACGTATAATGTTGATGAAATTGAGAATGTGATTAATGACGATGACATTGCTGA	tgaaacgtataatgttgatgaaattgagaatgtgattaatgacgatgacattgctga	ACTGAAATAATCCAAAAAACACATTGAAAGTATCCTTGCTGATAAGAGATTGGATG	aatactgaaataatcccaaaaacacattgaaagtatccttgctgataagagattggatga	TCAACAGAATCCGACATTCAATCGAAAAATGAAATATCACCAGTGATTAATGAGAA	aattcaacagaatccgacattcaatcgaaaaatgaaatatcaccagtgattaatgagaa	AG -	totootattaattagttagtgatcatactgaacttgotacagactcgggaaatgatag	ΑT	cttaatgaacaaactgatatagttgatactgttgctaaagttattgagaatgaaaaaat		gaaacagaggatgctggtaacagtccaattcaagacgaagtttctcaagagggaagaat	AATGT	tttccggggggtgatgatgattctgtcgtgatcaactcaaatgttgagcaatctaatgt	CTCGTTACTGGCTAATAAGAATCGGGTAACTGAAAAAATAGATGAGGGAGAAAATATTTC	GAAGATTGGCATACTTCTGACTACCCAGAAACTAGTGCTGAAGATGAACAGCAAAATCC	agaagattggcatacttctgactacccagaaactagtgctgaagatgaacagcaaaatcc	GAGTCAAAATTGTCAGGAACAGATCATTTCGGTGTCGACGTTGTTAAAGAAACAGTCTC	ggagtcaaaattgtcaggaacagatcatttcggtgtcgacgttgttaaagaaacagtctc	TCGGA	gaatctactqctcagqttggactatcacaccaaccccagactggtactcccgcttcgga	GCCTATTACAAACCACAAAGGACGCCCCTTCCATCCAGGGGACGATAAACGCCT	cctattacaaaccacaaaggacgccccttccatccaggggaggga	TCCGGTGTCTAAACCTCCTCAACTTGGTACCGAGACTTCAGTAATAGGGAAGTCTAAAGA	ccggtgtctaaaacctcctcaacttggtaaccgagacttcagtaatagggaagtctaaaaga
4500	4440		38			4260	4260	4200	4200	4140	4140	4080	4080	4020	02	9	3960	3900	9	8	4	3780	78	3720	66	66	6	3600	3540		3480	4.8	3420	3420

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ACCESSION VERSION

AF050215.1

GI:3273716

polyprotein (pol) genes,
AF050215

SOURCE KEYWORDS ORGANISM

Candida albicans Candida albicans

RESULT 2
AF050215
LOCUS
DEFINITION

AF050215 6980 bp DNA Candida albicans Tca2 retrotransposon gag polyprotein (gag) and

pol

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JOURNAL
REFERENCE
AUTHORS
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Goodwin, T.J.D. and Poulter, R.T.M.
Temperature and strain-dependent expression of the pCal
retrotransposon of Candida albicans
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EQSNVETEDAGNSPIQDEVSQEGRILNEQTDIVDTVAKVIENEKISPINSLDDHTELA
TDSGNDSNSTESDIQSKNEISPVINEKNTEIIQKHIESILADKRLDEFETYNVDEIEN
                                                                                                                                                             EGIITKDRKVKÖLLIQRLKIWNNRFNDKVAYFRSDNAPEFPQPSDLAEFFGIWRETIAA
YSPELMGLAEVVNKLIQQIYAIVYTLGPGIIKLIYYVYQQYSIMYINHTPRRSIKGQT
PYGCYYQLSEGNEYRPFALIOCVTESNAIEKRRYGVTSTKGAPSSIMGAVIGYASOC
FSYYVLLKNMRCDIILSPNVRILRSYEVINSYLKNLSTTPMSHIVPMAEGIQGROSGA
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DVEISPYGVEQLLPTGDKNDIYNFHLMSNHMSIEKILLLQKYQGLVLHTSKESLQKIA
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/protein_id="AAC24820.1"
/db_xref="GI:3273717"
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                                                                                 <u>EPITNHTKDAPSIQGRDHKRSESTAQVGLSHQPQTGTPASEESKLSGTDHFGVDVVKE</u>
                                                                                                                                 QYEVRGTYVESEYDNTNDVMHMPKESYSVQPASFTLTTGNSSNEYVINDDPVQITIEN
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/protein_id="AAC24821.1"
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/chromosome="3"
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cgtcggtaatcagaaaagcgtggataaatggaatgaagaatttaaaatatttccacgttgc
                                                            ACATATCAAGGCTAGATTCAATATGCTTTTCATAAAATTTAATGACTTACCTAAGTTGGC 746
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/note="3' tarr^^
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6353. .6632
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LIYCLRYIKNSMGYHIEYKRNRLNIPPKSFVIECFSDASFAPGLDRKSISGTLIYVNG
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RKSRCVVHGNRQKEKLDYDPFSVSSPVIDLVTIRLLTIIGCELGMTIQHLDVESAYLN
ASITHSNPIYVFPPKSVPLKKNHCWLLKRSVYGLKQSGFEWYHTIKRVLEDIGFNQVL
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TDPREAIRVLNTGETKRIEPKKREVPITVKLNKRSQYKSPYVTRSGRTVINPKRYLHA
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3661. .3671
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1587. .1661
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at 2640 AT 2846	1 tyttaataaattyattttacaacagatttacaggatcyttytyacacttyytccacaa 	Qy 258 Db 278	
gt 2580 GT 2786	1. cggtatttggagggagactatagcggcatatotgcctgagcttaatggtctcgccgag 	7 5	
tt 2520 TT 2726	1 ggcatacttcagaagtgataatgctcctgagttcccacaaccttctgatttagctgag 	24 26	
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5006	TTGACATAATAGGTTGTGAATTAGGAATTGACAATTCAACATTTAGACGTCGAGTCGG	4947	Db
4800	attgacaataataggttgtgaattaggaatgacaattcaacatttagacgtcgagtcggc	4741	Qy
4946	GATTATGACCCTTTTAGTGTTAGTTCACCTGTTATAGATCTTGTGACTATAAGATT	4887	Db
4740	ttggattatgacccttttagtgttagttcacctgttatagatcttgtgactataagatt	4681	Qy
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62	aattcccaccggtgtgaagcctatatctatgggttgggt	U	Qy
4766	TTAGATCAAAAGATGTTTACGAAGAAGTTCC	4707	Db
4560	aagtcaatgaatgctgaactagagaaatttagatcaaaagatgtttacgaagaagttcc	4501	Qy
4706	CCCCAAGAGGTATTTACATGCGGTCGTCAACAAAATCGACTATAATGATCCGGGATGGAT	4647	Db
4500	cccaagaggtatttacatgcggtcgtcaacaaaatcgactataatgatccgggatggat	4441	Qy
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4440	aacaaaagatcgcaatacaagtcaccatatgttacaagaagtggtagaacggttataaa	4381	VΩ
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4380	actggtgaaaccaagagaatcgaacccaagaaaagagaggtgcctatcactgtgaaat	4321	Qγ
4526	TGCTGGTACTAAACATTCACTTGATACAACTGATCCAAGAGAAGCAATCAGAGTGTTAAA	4467	Db
4320	gctggtactaaacattcacttgatacaactgatccaagagaagcaatcagagtgttaa	4261	Qy
46	TCATAGCATGTCACGAGCAAAGAAGAAATACACATTTGAGAAAGAA		Db 4
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4200	agctaatccactaccagatgaaaataatgatgttcagatgatgatgagaggttttgataataa 	4141	D Oy
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4	atttgaaacgtataatgttgatgaaattgagaatgtgattaatgacgatgacattgctga	4081	Qy
4286	AAATACTGAAATAATCCAAAAACACATTGAAAGTATCCTTGCTGATAAGAGATTGGATGA	4227	Db
4080	aatactgaaataatccaaaaacacattgaaagtatccttgctgataagagattggatga	4021	Qy
4226	TTCAACAGAATCGACATTCAATCGAAAAATGAAATATCACCAGTGATTAATGAGAA	4167	Db
4020	aattoaacagaatcogacattcaatcgaaaaatgaaatatcaccagtgattaatgagaa	3961	Qy.
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Submitted (07-DEC-1999) Del Rey F.,
Genetica, Universidad de Salamanca,
Salamanca, 37007, SPAIN
                                                                                                                                                                                                                                                                                                                                      Cloning and characterization of the endo-1,3-beta-glucanase-encoding ge
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/transī_table=12
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711. .4148
                                                                          /gene="engl"
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/strain="ATCC64385"
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Matches Query Match Best Local COUNT 6175 4752 6115 6055 4452 6415 4512 4572 6295 6235 4692 4812 5995 taagtgtctaagtcgtgctaaattcaaagcattcgttgagggtatgataaaacggttaga 6054 source 4872 TAAGTGTCTAAGTCGTGCTAAATTCAAAGCATTCGTTGAGGGTATGATAAAACGGTTAGA 4813 source aaactgatcaatgaaaatgatggttattatgagaatggaaaatttttccatcacacatca 6234 attactattatcgtaatgctcaatcaggggagtgttggtttgttgcactattttgtgtcag tatattccatca ATTACTATTATCGTAATGCTCAATCAGGGGAGTGTTGGTTTGTGCACTATTTTGTGTCAG CCTAGAAGATAATCAAACACTGATACAAAATGCAATAACGGCAGAATAAGTGGATTTATC 432; TATATTCCATCA 4441 Similarity 100. 32; Conservative 1569 complement(4441 ...4720)
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4721 ...4872 PAGVDNNGKPIGTNKFYTNLLLGNQDFMVYPLPYGLYWSKTSYYGFAVQHNNVSDRVFGSINTNNKGVASYYFNPTNNAELIFSAISFSKDSMHMKYSQMAELSALVTLSSSSNDE SNYLLDIPLVQGMGFVFGIYNGNLIPLLNSLFGVKDLSLETDALLENVLKYRATSLDD SNYLDIPLVQGMGFVFGIYNGNLIPLLNSLFGVKDLSLIQVAIAPEDNDNDKYYDAAAGM VVTGATVSGSVSQGTAASYKFSYTTAGKSSSNNPIVFALPHHMDSLTGSALDALTGIT VTSTTKGEMTGFLTNELEFSETINQDVEFLPWTENMTGSLTYTKDQLELLASAANKEL KSTYTSDISNNSQNRSSLSLTSTIDQLASITNSTLTTITKPTSLYPDFSYTNSSRYSS TMRNSSEESSMYLEKSSSKLLSSTSSLNSSSIASTTESSELASATTSDSSLSHSSSSS VELSSSLSSEADSSSSSESVETGSSDETASNYSGDLFKAIDTNAPPTVFARSEIPLTI DNVDSGWTGILRLNQALFDPKSSYEFFASNNWDDKWLDNGQSRTWSLAFAAGÂLNAS" 4441. .4720 ESLHFAAAIKLWGKVVGDQSMEARGGLMISIMARSFNMYFYYKSDNTVEPKQILPNKV SGIFFENKVDYTTFFGTPADHPEYVHGIHMLPITPSSSLVRKTSYVQEEWKDQIAGFI /translation="MLFKSVLLSTLIAVQALAENSAHQETVPYKTTHISNPCLENYAKKLLPNNPGTGLTTGIPTUTYAPQQDPNQVKQSESLQPTQSSKAQQQQQIQGSSVPASHLLPNPTGITTTGIPTTTQKQVCTVKTFSTIISHSESPTTTTTKQNEEKSIADTKSTKTTKTTTSTVFSATSLPSTTYTPSTSVSLVSTTKKN /db_xref="taxon:5476" 926 c 790 g /organism="Candida albicans" /transposon="pCal" GGTWAQSNKDWVNSLVRDASNPSADDTYFPVSRMFDWFSGHSWATGLFVTYKNIESSS AADIAATYKNMNSNYFSGKYLDKYAQILLVYSEIIQDEEYTKDALNAMKDAFKYFTQN KQYYPLMYDTKFGGVTSTSAQDGDPNADFGSAYYNDHDFHYGYFIHAAAIVGYYDKKL PVSSQSVVSTTKTISINTSLITDAVTITKEATTLPNSKHSSTFTNGSISFISTSANKV /organism="Candida albicans" /strain="ATCC64385" 6426 6.7%; >--100.0%; Pr 100.0%; 0; Score 432; DB 14; Pred. No. 4.9e-60; 790 g Mismatches 0; Length 4872; Indels 0; Gaps 4513 4633 6174 4753 6414 6354 4573 6294 4693 0,

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                                                               aatcatttcgtcccaaattagcgttgtataaattcagtcctcagatttgtattattgatt 360
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                                                  AACCATTTCGCCCCAAATTAGCGTTGTATAAATTCAGTCCTCAGATTTGTATTATTGATT
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403; Conservative
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Temperature- and strain-dependent expression retrotransposon of Candida albicans
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Goodwin, T.J.D. and
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/note="Perfect match to internal region of Candida
albicans transfer RNA-Arg-HCH"
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    tactgagaaaattgattctctcaaaggtgttgttcggaaatcacgttgtgttgttccatgg 4662
                                                                                                                                                                       taatgatccgggatggataaagtcaatgaatgctgaactagaggaaatttagatcaaaaga 4542
                                                                                                                                                                                                                                                    t99tagaacggttataaaccccaagaggtatttacatgcggtcgtcaacaaaatcgacta 4482
                                                                                                   tgtttacgaagaagttccaattcccaccggtgtgaagcctatatctatgggttgggtaca 4602
                                                                 AGTTTACACCGTTGAAAAAACACCAAAGAACGTTGTCCCATTGAAAACCATGTGGGTACA 180
                                                                                                                                                CAATCAAAAAGAATGGCGTCAAAGTATGGAAGAAGAAATCGAAAAATTTAAGGCTAACCA 120
                                                                                                                                                                                                                             TGGAAGATCAGTGCATCCACCTAAAAGATATTTAAATGCCATTGTTAAGAAAATAGATTA 60
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AF078809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tca4, a Ty1-copia retrotransposon Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goodwin, T.J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida. 1 (bases 1 to 1470)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="reverse transcriptase"
/product="reverse transcriptase"
/protein_id="AAC28090.1"
/db_xref="0ci:337679"
/db_xref="0ci:337679"
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EKTPKNVVPLKTWWVHTYKTNDLKHNYKSCLVVWMGNVLWENRDPDPHAISSPVVDLT
SIRLLSAIAVENNLVHGVDI JASAYLNASLEOGRYIFVREPPRGEEVKFGYSWRLHKSV
YGLRQSAHNWYSHFKNVLEANGLKQTLHNDGIFWKNYENGDVLYVSVYVDDVFMIATN
EKIIKEEVAMLETYFQLQYFGEATEYLGJQFRKTPDGYIFPLEKLVATFNIQDS
EKIIKEDVAMLETYFQLGYFGEATEYLGJQFRKTEDGYFLTDQIFPLEKLVATFNIQDS
YGKDIFIIFKDINVYKQLKKSSQINDFWKLEKOPKLINSVSKTKYIDDYEENEEHDFK
ESPQAEPLSAKGIKLYQSAVGSLLWASMNTRPDLAFSVNQLGAKCAHPDVDDWKRLMY
CLRYIKKDMDFKLEYKGGRLNNKSKDFIIECFSDASFAPDLDRKSITGTSIFVNGNLV
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Location/Qualifiers
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241 c 299 g 408 t
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<1. .>1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Tca4 retrotransposon"
/rpt_family="Ty-1-copia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Candida albicans"
/strain="SC5314"
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Pred. No. 4.3e-45;
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TATTGAATGTTTCTCAGATGCCTCATTTGCCCCAGATTTGGACAGAAAGTCAATCACCGG
                     tatcgaatgtttcagtgatgcgtcatttgcaccaggattggatagaaaatctattagtgg
                                                                              TATGGACTTCAAACTTGAATACAAGAGAGGGAAGACTCAACAACTCAAAAGATTTTAT
                                                                                                        catgggatatcacattgagtacaaaaagaaacagattgaatataccaccaaaaatcatttgt
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                                                                                                                                                             attgcttgaccctgatgctaaaaaactataccaaagtggtgtttggcctgcttttatgggc
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                                                                                                                                                                                                                                                                                                            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotlin-Fukuhara, M., Bon, E., Brottier, P., Casare, C., Llorente, B.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1)
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Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                              /note="end : T7" <1. .>1017
/evidence=not_experimental
177 c 158 g 313
                                                                                                                               /db_xref="taxon:4959"
/clone="BCOAA012E08"
/clone_lib="BCOAA"
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/strain="CBS 767"
                                                      /note="part of putative transposable element"
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RESULT AX073190

DEFINITION

AX073190 Sequence AX073190

301 from

Patent W00102550.

1888

AX073190.1

REFERENCE

AUTHORS

Contreras, R.H.,

de Backer, M.D., Luyten, W.H.,

Malcorps, I.K.

(bases 1 to 1888)

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

Candida albicans

Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic

Saccharomycotina; Saccharomycetes;

Saccharomycetales;

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                     ttgaatttcgtaaaaccgaatctggttatattttatctcaagaaaaatttctcaa 5217
                                                                                                       atcaattgagagatcattttgaagttaaagtgtttggtgaaatatcaaattatcttggta 5162
                                                                                                                                                                                                                                                                                acacaatgatggtttatttcacattgaatatgaagagggatcagtaatatat-ttaggtt 5042
                                                                                                                                                                                                                                                                                                                                                    tttggaatggtatcacactatcaaaagagtattggaagacattggttttactcaagtttt 4983
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TTGAATTCATTCAAATTGCAGGGGGGTATAGATTATCACAACACAATTTCTTGAA 1017
                                                                                                                                                              TATATGTGGATGATATGTTTTTAACTTCGTCTAATATTACAATTCTTAACGATTTCAAAC 902
                                                                                                                                                                                                                                            TGCCATTAGCGGAATGTTTTGTAAATATTTTGAGTGAAAATAAGAAGCTCATCGTTGCAC 842
                                                                                                                                                                                                                                                                                                                                                                                                         tctaaatgcctctattactcattcaaatccaatttatgtctttcctcctaaatcagtacc 4863
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                    Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                                                                                                                                                                                                                                                                                                                                                                       Souciet, J.L., Aiglé, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies(1) TEBS Lett. 487 (1), 3-12 (2000)
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T3 end of clone EC0AA003C05 of library BC0AA from strain CBS 767 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepingle,A., Casaregola,S., Neuveglise,C., Bon,E., Nguyen,H., Artiguenave,F., Wincker,P. and Gaillardin,C. Genomic Exploration of the Hemiascomycetous Yeasts: 14. Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)
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                                                                                                                                                                                                                                                                                Direct Submission
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Debaryomyces hansenii
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Saccharomycetales; Saccharomycetaceae; Debaryomyces
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Local Similarity 51.0%;
                                                                                                                                                                                      acacaatgatggtttatttcacattgaatatgaagagggatcagtaatatatttaggttt 5043
TGAACTCGCTAAACATTTCG 905
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the other extremity of this insert.
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                                                                              gtcaatgaatgctgaactagagaaatttagatcaaaagatgtttacgaagaagttccaat 4563
                                               GTCAATACAACGCGAATTAGATACTTTTAAGAAATATGAAGTATATACGGTTGTGAAAAT 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY Cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. vvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Debaryomyces hansenii.
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end of clone BC0AA006C12 of library BC0AA from strain
baryomyces hansenii, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="end : T7" <1. .>838
                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
162 c 128 g 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="BCOAA006C12"
/clone_lib="BCOAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Debaryomyces
/strain="CBS 767"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /variety="hansenii"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="part of putative transposable element"
                                                                                                                                                                                                                                                   2.0%; Score 127.2; DB 5
49.8%; Pred. No. 4.7e-11;
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                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 80561)
Town, C.D. and Kaul, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequence AC073555
                        submitted (30-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Jan 30, 2001 this sequence version replaced gi:12320681.
                                                                                                                         submitted (19-JaN-2001) The Institute for Genomic Research,
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.or,
4 (bases 1 to 80561)
Town,C.D. and Kaul,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Utass,B.J., Wu,D., Malti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F1114 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                        Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                   Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
3 (bases 1 to 80561)
                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUN-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 80561)
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                                                                                                                                                                                    cdtown@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                                                                                                                                                                         DPLKATTHPLAFDGEENNREFKNLGPSEWGHQFLSAHVDLSEMDALEREIEALKPKVR
DMLISSESSKKKILFIVILVSLGLAVHFEDEIXESLEDGLQKIEEMMASEDDLRFKGD
NGKFKECLAKDAKGILSLYEAAHMGTTDYILDEALSFITTYMESLAASGTCKINLSR
RIRKALDQPQHRNMEIIVAMKYIQFYEEEEDOOKTLLKFAKLMFKFLQLHYLQELKIL
SKWYKDQDFKSKLPFYFRDRLVECHFASLTCFEPKYARARIFLSKIFTVQIFIDDTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNTEYKVEAFSAVYKKLTGKDVVFEFFITEA"

complement(join(<2677. .2964,3055. .3303,3412. .35)
4553. .4771.4862. .5230,6284. .6492,6561. .>6815))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to 40S ribosomal protein S7 homolog GI:5532505 from (Brassica oleracea)"
join(1109. .1183,1260. .1333,1447. .1570,1805. .1987,
                                                            QVAKWVKAGHLPSFDEYLDVAGLELAISFTFAGILMGMENVCKPEAYEWLKSRDKLVR
GVITKVRLLNDIFGYEDDMRRGYVTNSINCYKKQYGVTEEEAIRKLHQIVADGEKMMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2677. .6815)
/gene="F1114_2"
                                EEFLKPINVPYQVPKVVILDTLRAANVSYEKDDEFTRPGEHLKNCITSIYFDL'
                                                                                                                                         {\tt RYASLGEVESLADTIERWDPDDHAMDGLPDYLKSVVKFVFNTFQEFERKCKRSLRINL}
                                                                                                                                                                                                                                                                                                                                                                   /product="terpene cyclase, putative"
/protein_id="AAG60130.1"
/db_xref="G1:12597819"
/translation="MEAIRVEGLKLGSKLSIHSQTNAFPAFKLSRFPLTSFPGKHAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(2677. .2964,3055. .3303,3412. .35,4553. .4771,4862. .5230,6284. .6492,6561. .6815))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MFSAQHKIHKEKGVELSELDEQVAQAFFDLENTNQELKSELKDLYVNSAVQVDISGGKAIVVNVPYRLRKAYRKIHVRLVRELEKKFSGKDVILIATRRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="40S ribosomal protein S7 homolog, putative"
/protein_id="AAG60128.1"
/db_xref="GI:12597817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F1114_2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to terpene cyclase GI:9293912 from Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F11I4_2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1114.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
/chromosome="I"
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/cultivar="Columbia"
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/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="AT_rich"
complement(5793...5755)
/rpt_family="AT_rich"
complement(6117...6171)
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complement(12467. .]2510.
/rpt_famil..."
                                                                            /Product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical protein"
/product="hypothetical"
/product="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13575. 13612)

complement(13575. 13612)

/rpt_family="AT_rich"

join(<14617. 14730,15176. .15240,15336. .15411,15494. ...
15850. .15944,16074. .16176,16261. .16307,16462. .16789,
17116. .17205,17304. .17366,17451. .17519,17652. .17714,
17804. .17856,17945. .>18119)

/gene="F1114_4"
PESVNENNLIRQPSPPPVLAEVQDLVPALCPEVREPECMIENSLPDESLRSESPLELHIATSMMDTFMRLAKSNTKKNLETCGILAGSLKNRKFYITALIIPKQESTSDSATNEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted by genemark hmm"
join(14617. .14730,15176. .15240,15336. .15411,15494. .19
15850. .15944,16074. .16176,16261. .16307,16462. .16789,
17116. .17205,17304. .17366,17451. .17519,17652. .17714,
17804. .17856,17945. .18119)
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/rpt_family="AT_rich"
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/rpt_family="AT_rich"
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EYLDVAGVEIAVYFTVAGILLGMENINKKEAYEWLIFRDKLVRAMSTKARLVNDLFGY
KDDMRRGYVTNSINCYKKQYGVTEEEAFRKLHQMVADGDKMMNEEFLKPINVPHQVLK
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/protein_id="AAG60132.1"
/protein_id="AAG60132.1"
/protein_id="AAG60132.1"
/db_xref="GI:12597821"
/translation="Meal RIVEGPKLGSRLSIRSHTTAFPACKLSREPLTSFPGKHAHL
/translation="Meal RIVEGPKLGSSEMGNQFLFAHVDLSEMDALEREIEALKPKVR
DMFMSSFKGMKSNKKNLFLIVLVSLGLAHHFEDEIEESVKGCSQEMVEMMDGENDLYT
VSIIFWVFRTYGHNISSDIFNLFKGHHKFKECLATDAKGILLYAKEYIRFYEQEEDC
DKTILEFSMLNLKFLQLHYLQELKLLTKWYKEQDFESKLPPYYRDRIVELHLATLAYI
DEALSFTLSYLESLAANGTCKPNLVERIRNALGLLQNKNVESILVAKEYIRFYEQEEDC
DKTILEFSMLNLKFLQLHYLQELKLLTKWYKEQDFESKLPPYYRDRIVELHATLAYI
NFKYSRVRILLTMIYTIQIILDDTCDRYASLREVESLAATIERWDHNDHAMEGLPDYL
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/gene="F1114_3"
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/gene="F1114_3"
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Matches 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45865 TGGAGAAATGCCATGGATGAAGAGATCAAATCAATACAAAAGAATGACACATGGGAGTTA 45806
                                                                                                                                                                                                                                                                                                                                                                                                                                          45448 CAAGCCCCAAGAGCTTGGAAT-ACTCGAATTGACAAGTATTTCAAGGAGAAAAGATTTCAT
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  5216 aagaaattacttaaggatttcaaactagatgactcatat 5254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTCT---AAAGGAGAAGTGGAAAGATACAAAGCAAGATTGGTTGCAAAAGGTTATATT 45689
                                                                                                                                                                                                                                              GCATGCTTATATGTAGATGATTTGATATTCACGGGTAACAATCCAAGCATGTTCGAAGAA 45272
                                                                                                                                                                                                                                                                                        traggttratatgttgatgatattcttatggttggaagttcacaaaaagttattgataat 5095
                                                                                                                                                                                                                                                                                                                                             CAAGTGT--CCATATGAGCATGCACTCTATATCAAAAATTCAAAAAGAAGATATATTGATC 4533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAGTCAAAGGTGAAGAAGACAAAGTCTTGAGGCTAAAAAAGGCGCTTTATGGATTAAAA 45449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agattattgacaataataggttgtgaattaggaatgacaattcaacatttagacgtcgag 4795
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                                                                                                                                                                                                                                                                                                                                                                                        caagttttacacaatgatggtttatttcacattgaatatgaagagggatcagtaatatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGGCCTTCTTAAATGGAGATCTTGAAGAAGAAGTTTACATTGAGCAACCACAAGGCTAC
                                                                                            cttggtattgaatttcgtaaaaccgaatctggttatattttatctcaagaaaaatttctc 5215
                                                                                                                                                 TTCAAGAAAGAGATGACAAAGGAGTTCGAGATGACGGACATTGGATTGATGTCTTACTAT
                                                                                                                                                                                            ttgtggatcaattgagagatcattttgaagttaaagtgtttggtgaaatatcaaattat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcagtacctttgaagaaaaaccattgttggttattgaaacgttctgtctatgggttaaaa 4915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              toggogtatotaaatgoototattaotoattoaaatooaatttatgtotttootootaaa
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/note="predicted by genemark hmm"
complement(19300. .20055)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLSPQPLPTKHSEKETNGRASGANSDSEAEKSSKSFWSFKRSSSLNCDIKKSLICSFP
RLTRSNSTGSVTNSKRAMLRDVNNHRPSSRSSCCNAYQFRPQKHTGKKGEGGGSFSVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="AAG60135.1"
/db_xref="G1:12597824"
/translation="MICTEALQRISESSDLGQSDKAPPPVIEPSGLIRRDETLLDSSN
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    Mismatches

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Pred. No. 8e-07;
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REFERENCE
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ATT20K12/c
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Arabidopsis
AL137898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer Submitted (31-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemckedmips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project lemckedmips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 109155)
De Haan, M., Maarse, A.C., Grivell, L.A., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaston Cremieux, BP191, 91006 Evry Cedex, France;
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550. .640
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521. .549
                                                                                  /www.e="23 bp poly(T) tandem repeat" complement(6549. .6636)
                                                                                                                                                 2303.
complement(join(6549.
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/gene="T20K12.10"
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/gene="T20K12.10"</pre>
                                                                                                                        2303. .2325
/note="23 bp
                                                                                                                                                                     /note="inverse repeat of region bp no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTVFSHSQTVVVCGNCQTILCQPTGGKAKLTEGCSFRRKGD"
                         /gene="T20K12.20"
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                                                                                                                                                                                                                                           /gene="T20K12.10"
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/db_xref="GI:6850878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ribosomal protein S27"
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/gene="r20K12.30"
10685..11011
/gene="r20K12.30"
/number=1
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                                                                                                                                                                                                                                                                                                      /translation="MALKRGLSGVNRIRGSGGGSRSVLVLLIFFCVFAPLCFFVGRGV
YIDSSNDYSIVSVKQNLDWERKLAMGSVRSLFSKEILDVIATSTADLGFLSLDSFKKN
NLSASWRGTGVDPSFRHSENPATPDVKSNNLLMEKRDSISKDSIHQKVETPTKIHRRQL
REKRREMRANELVQHINDDTILKLENAAIERSKSVDSAVLGKYSIWRRENENDNSDSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB71042.1"
/db_xref="GI:6850879"
/translation="MGRGKVPUKRIENKITRQVTFSKRKSGLLKKAYELSVLCDAEVS
/LIFSTGGKLYEFSNVGGRTIERYYRCKDNLLDNDTLEDTQGLRQEVTKLKCKYESL
LRTHRNLVGEDLEGMSIKELQTLERQLEGALSATRKOKTQVMMEQMEELRRKERELGD
INNKLKLETEDHDFKGFQDLLLNPVLTAGCSTDFSLQSTHQNYISDCNLGYFLQIGFQ
QHYEQGEGSSSVTKSNARSDAETNFVQ"
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/note="non-consensus GC donor site at position 7295 and 7551, additional T in poly(T) stretch leads to discrepancy of as sequence to published protein; Contains MADS-box domain signature and profile AA3-57; Prokaryotic membrane lipoprotein lipid attachment site AA180-190"
                                                                                                                                                     KKDIENÄÄVVHYNGNMKPWLELAMSKYRPYWTKYIKFDHPYLRRCNLHE"
                                                                                                                                                                                       {	t PLWEVNLNGKVNGAVETCGESFHRFDKYLNFSNPHIARNFNPNACGWAYGMNMFDLKE}
                                                                                                                                                                                                         EYYFKADHPTSGSSNLKYRNPKYLSMLNHLRFYLPEVYPKLNKILFLDDDIIVQKDLT
                                                                                                                                                                       WKKRDITGIYHKWQNMNENRTLWKLGTLPPGLITFYGLTHPLNKAWHVLGLGYNPSID
                                                                                                                                                                                                                            KHVFHLVTDKLNFGAMNMWFLLNPPGKATIHVENVDEFKWLNSSYCPVLRQLESAAMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similarity to several hypothetical proteins
Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(7799.
/number=7
                                                                                                                 /gene="T20K12.30"
                                                                                                                                                                                                                                                                                                                                                                                   /product="putative protein"
/protein_id="CAB71043.1"
/db_xref="GI:6850880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(10534..10684,11012..11037,11137..11196,11287..1
11502..11565,11643..11689,11804..12138,12233..12590,
12701..13279,13374..13649)
/gene="T20K12.30"
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                                                                                    85664 CCAAAAAGCCATTGAAAAGAAGACTTGGAGAAATGCCATGGATGAAGAGATCAAATCAAT 85605
                                  4531 tagatcaaaagatgtttacgaagaagttccaattcccaccggtgtgaagcctatatctat 4590
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Arabidopsis thaliana chromosome
Direct Submission
Submitted (19-AUG-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
                                                                                                                                                                                        Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/) Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named indicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.or. On Jan 19, 2001 this sequence version replaced gi:12280859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 1 to 85961)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://genemark.biology.gatech.edu/GeneMark/), GlimmerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prediction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC clone T18I24 is from Arabidopsis thaliana The orientation of the sequence is from SP6 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                           /note="similar to auxin induced transcription factor GI:5731257 complement(2159...3364) /gene="T18124.2"
                                                              transcription factor,
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/db_xref="GI:12321381"
                                                                                                                                                                                                                                                                                                     complement(2159. .3364)
/gene="T18124.2"
                                                                                                                                                                                                                                                                                                                                                      complement(<2159.
/gene="T18I24.2"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYSVFEFATNAWKVTDHTRFHEKPELMDDSGRVSLNGNLYWTAYNSPHTGQYFIAMLD
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LNGGGGVVWNPLFWRQTKWIAKAENTCGKAIGYDGSRPEKSYKIIGRSSCSWQGKVTD
                                                                                                                                                                                                                                                                                                                                                                                                          YIVRGDLCKKIKIDQVLCEFQSSVYVPSLITIP"
                                                                                                                                                                                                                                                                                                                                                                                                                                          GNGDDGDDVVWIKFMTVSRPDFPILLSYISTSYFVDNDIHGKSFVLCCPSKRPKAAWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein, 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1. .1104
          /translation="mdlsdiknnnndtaavatgggarqlvdaslsivprstppedstl
attsstatatttkrstkdrhtkvdgrgrrirmpalcaarvfqltrelghksdgetiew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to unknown protein GI:2262162 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T18I24.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="mi259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Arabidopsis thaliana"
                                                                                                                                             /product="auxin-induced basic helix-loop-helix
                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .>1104
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complement(14034...14074)
/rpt_family="AT_rich"
complement(14182
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEIQRMRQLMSLWSNLKSSRVSLTGGNHTAASSADTFLKASRSE
VISLEMSSTLLALLFLSFTWISSLKYGTTATARSKSVESDLFELLPLLLNDLEKQGLF
KMGDKALFLSGGDDEYVYSSYSQTVIETDMLLVSASDQEMQSMVPDETDFAFAHSRH
IDSAEFIDRTLKVGGIFTVQLMLQDLPNFLKHPNYELVYVKSSEYTVMTMKKTGETE
QKQSLVATGRKLLGITEEDAREKALRKLEDVLLEPPRAASRKSRTYFKRTRYLPDLMG
                                                                      complement(<14901. .>18863)
/gene="T18I24.5"
                                                                                                                 complement(14182. .14205)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(8599. .8627)
/rpt_family="AT_rich"
join(<10149. .10243,10536. .>11703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to bZIP transcriptional activator RSG GI:8777512 from (Nicotiana tabacum)" complement(join(5299. .5357,5415. .5651,5738. .5864 .5048. .6043,6135. .6853))
/note="similar to copia type polyprotein GI:6850900 from
                           complement(14901 .18863)
/gene="T18I24.5"
                                                                                                                                                                                                                                              /pseudo
                                                                                                                                                                                                                                                                       /note="pseudogene,
factor HSF30"
                                                                                                                                                                                                                                                                                                               complement(12815. .13163)
/gene="T18124.17"
                                                                                                                                                                                                                                                                                                                                                           /rpt
                                                                                                                                                                                                                                                                                                                                                                               complement(10335
                                                                                                                                                                                                                                                                                                                                                                                               KSGRAYWECLALYGKLRDEGVAVHQWWG"
                                                                                                                                                                                                                                                                                                                                                                                                                 {	t GMTEWLKENVKEEEYVVMKAEAEMVEEMMRSKSIKMVDELFLECKPKGLGLRGRKMQS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Join(10149. 10243,10536. 11703)
/gene="T18124.4"
/codon **----
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GRLRALYQQQQTQKPSASRGRATSKDLDSQFSSLSLNTKDSNCRRDSVSVMGPGDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLDVANATNISLTLQNDFSYRNTVLSTQRGVQELDRNKNAQDAAFYSGASFLKQKSRQ
RDSLVATGACPSWLPFARENGGGKNLGALYMSQDATVISSERKNYAEPFSHDPKMLSS
EENNSNPSPVTYEADNTKRAKQQFAQRSRVRKLQYISELERNVQTLQAEGSKVSAELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSRHGQKLSNEKTHHQRTSSESHLVEELPFWLDDLLNEQPESPARKCGHRRSSSDSYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(<5299. .5357,5415.
5968. .6043,6135. .>6853))
/gene="T18I24.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4594. .4638)
/rpt_family="AT_rich"
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EQGGGGVFAAHTSPLLGFHHQLQHHQNQNQOPVETIPEGENESRKKYRSVDLSKEN
DDRKQNENSLKESETSGEPTAAPMAVAPPSRSKGAGNTFWHLPVFTTAAQNGESSSNU
NTAACHRAPPMWPFVNSAGGGAGGGGAATHFMAGTGFSFPMDQYRGSPLQLGSFLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNLDLESYSRRVFIDVGNGKGSSGMEWFVENYPTRNQKFEMYKIETVNDEMSLESEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAG50763.1"
/db_xref="GI:12321385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
/protein_id="AAG50761.1"
/db_xref="GI:12321383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(5299. .6853)
/gene="T18I24.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MASSKGSQSVRNLMYPGKHALLPPKIPFPSVSASYSEYIPTGLI
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ement/8500
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complement(16191. .16412)
                                                                                                                                                                                                            KDFIKCPYEHALYIKIQÄEDILIACLYVDDLIFTGNNPSMFEEFKKEMTKEFEMTDIG
LMSYYLGIEVKQEDNGIFITQEGYAKEVLKKFKMDDSNPVCTPMECGIKLSKKEEGEG
VDPTTFKSLVGSLRYLTCTRPDILYAVGVVSRYMEHPTTTHFKAAKRILRYIKGTVNF
                                                                                                                                                                                                                                                                                                                                                 QIEEKCEPMDFQEAIEKKTWRNAMDEEIKSIQKNDTWELTSLPNGHKAIGVKWVYKAK
KNSKGEVERYKARLVAKGYSQRAGIDYDEVFAPVARLETVRLIISLAAQNKWKIHQMD
VKSAFLNGDLEEEVYIEQPQGYIVKGEEDKVLRLKKALYGLKQAPRAWNTRIDKYFKE
                                                                            AEYVAATSCVCHAIWLRNLLKELSLPQEEPTKIFVDNKSAIALAKNPVFHDRSKHIDT
RYHYIRECVSKKDVQLEYVKTHDQVADIFTKPLKREDFIKMRSLLGVAKSSLRGGVES
                                                                                                                                                                      GLHYSTTSDYKLVGYSDSDWGGDVDDRKSTSGFVFYIGDTAFTWMSKKQPIVTLSTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AWSGRKPGVSHLRVFGSIAHAHVPDEKRSKLDDKSEKYIFIGYDNNSKGYKLYNDDTK
KTIISRNIVFDEEGEWDWNSNEEDYNFFPHFEEDKPEPTREEPPSEEPTTPPTSPTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYYYIPSMKTNILSLGQLLEKGYDIRLKDNNLSIRDQESNLITKVPMSKNRMFVLNIR
NDIAQCLKMCYKEESWLWHLREGHLNEGGLELLSRKEMVRGLPCINHPNQVCEGCLLG
KQFKMSFPKESSSRAQKPLELIHTDVCGPIKPKSLGKONYFLLFIDDESRKTWYYFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EENGQSYQRRGGGQVRGRGRGGYGNGRGWRPHEDNTNQRGENSSRGRGKGHPKSRYDK
SSVKCYNCGKFGHYASECKAPSNKKFEEKANYVEEKIQEEDMLLMASYKKDEQEENHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENEGSLSQTQKDGLKDSKKRDKKALCLIYQGLDEDTFEKVVEATSAKEAWEKLRTSY
KGADQVKKVRLQTLRGEFEALQMKEGELVSDYFSRVLTVTNNLKRNGEKLDDVRIMEK
VLRSLDLKFEHIVTVIEETKDLEAMTIEQLLGSLQAYEEKKKKEDIVEQVLNMQITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="copia-type polyprotein, putative"
/protein_id="AAG50765.1"
/db_xref="GI:12321387"
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/gene="T18124.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PQQNGVAERKNRTILEMARSMLKSKRLPKELWAEAVACAVYLLNRSPTKSVSGKTPQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKSEVFEIFKKFKAHVEKESGLVIKTMRSDRGGEFTSKEFLKYCEDNGIRRQLTVPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MASNNVPFQVPVLTKSNYDNWSLRMKAILGAHDVWEIVEKGFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Arabidopsis thaliana)"
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1.5%; Length 85961;

Local Similarity TGGAGAAATGCCATGGATGAAGAGATCAAATCAATACAAAAGAATGACACATGGGAGTTA 16353 Conservative 0; Score 98; DB 12; Pred. No. 1.3e-06; 0; Mismatches 375; Indels 12; Gaps 4;

ACTTCACTTCCAAATGGACACAAGGCAATTGGCGTGAAGTGGGTGTATAAAGCAAAGAAA 16293 gttccaattcccaccggtgtgaagcctatatctatgggttgggtacatactgagaaaatt 4615

AACTCTAAAAGGAGAAGTGGAAAGATACAAAGCAAGATTGGTTGCAAAAGGTTATAGTCAA 16233

aaggaaaaattggattatgacccttttagtgttagttcacctgttatagatcttgtgact 4732

AGAGCCGGAATTGACTATGAC-----GAGGTATTTGCTCCCGTTGCTCGTCTAGAAACG 16179

ataagattattgacaataataggttgtgaattaggaatgacaattcaacatttagacgtc 4792

gagtcggcgtatctaaatgcctctattactcattcaaatccaatttatgtctttcctcct 4852 |||||||| GTTAGACTAATCATCTCACTAGCGGCTCAAAACAAGTGGAAGATACATCAAATGGATGTC

aaatcagtacctttgaagaaaaaccattgttggttattgaaacgttctgtctatgggtta 4912

TACATAGTCAAAGGTGAAGAAGACAAAGTCTTGAGACTAAAAAAGGCGCTTTATGGATTA 15999

AAACAAGCCCCAAGAGCTTGGAAT-ACTCGAATTGACAAGTATTTCAAGGAGAAAGATTT aaacagtcgggtttggaatggtatcacactatcaaaagagtattggaagacattggtttt 4972 15940

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTAAGGAGGTACTTAAGAAGTTCAAGATGGATGACTCAAAT 15660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCTCGGAATTGAAGTAAAACAAGAAGACAATGGAATATTCATAACTCAAGAAGGCTAT
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                                                                                                                                        GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tqi.shtml). Annotated genes are named to indicate the level of evidence for their annotated genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as the protein and the protein of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                                                       hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prediction programs including Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-JAN-2001) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-SEP-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org 3 (bases 1 to 103637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC T15M6 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC clone T15M6 is from Arabidopsis thaliana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                          http://ftp.genome.washington.edu/RM/RepeatMasker.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Town, C.D. and Kaul, S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BAC T15M6 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
complement(10552. .10573
/rpt_family="A"."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="AT_rich"
complement(6713..6740)
/rpt_familv=""-"
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/gene="T15M6.24"
complement(3557. .4729)
/gene="T15M6.24"
                                                                                                                                                                                      /note="contains similarity to cell proliferation related protein GI:931486 from (Mus musculus)" (2004), 19786. .19886 complement(join(18837..19207.19528..19647,19786..19886 20080..20291,20407..20787,20902..20989,21228..21288, 21891..22125,22758..22835,22952..23614))
                                                                                                                                                                                                                                                                                                                                                                                                                                       20080. .20291.20407. .20787.20902. .20989.21228. .21
21891. .22125.22758. .22835,22952. .>23614))
79ene="T15M6.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1091. .2595)
/gene="T15M6.25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(10552..10573)
/rpt_family="AT_rich"
complement(10742..10991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7047. .7147)
/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                                                                                   complement(18837. .23614)
/gene="T15M6.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcriptase"
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/gene="T15M6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
complement/1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /pseudo
complement(11760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELQGDSHRFKKGETYYVLSLIGLALSWQVWAVGLMGLVLYVSGVFGDVVHMCTSPLVA
LFVVLAFDFMDDEFSWPRIGTLIATVVALGSYFYTLHKRNKKKMVELYQTENNIDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAIFAAIINRFKFTRWIILSIIGSILIYVFGSPEFGGEPDENEEFYSIQAWLTFAASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown protein"
/protein_1d="AAG50699.1"
/brotein_1d="AAG50699.1"
/db_xref="G1:1321255"
/translation="MEMTEASKOTTAEGSANPEPDOILSPRRSLELKOKKWWISVSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(<3359. .>4729)
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/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/cultivar="Columbia"
   ENSELESKMEVDAPSPIAGSVDLADNIAAKSVARVKVKLKTSKAPEPNETLRDDIDKS
                                                             /product="hypothetical protein"
/protein_id="AAG50696.1"
/db_xref="GI:12321252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFALSLCLFQLCFEKVLVKTKRYGNKKVFRMVIEMQICVSFVATVVCLVGLFASGENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="pseudogene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="T15M6.23"
                                       translation="MKRKRGHKKGKKSKTINEQGNLNESTENAENQTSEHSSEAPVEC"
                                                                                                                                                         codon_start=1
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complement(32999. 33008)
/rpt_family="(TA)n"
complement(3353. 33276)
/rpt_family="(TA)n"
                                                                                                                                                                                                        Inote="contains similarity to maleless protein (mle) d1:157905 from (Drosophila melanogaster)" (M739,40922 ..41017, 41217 ..41405,41490 ..41576,41787 ..41853,41997 ..42067, 42272 ..42409,42496 ..42597,42686 ..42769,42978 ..43034, 43117 ..43206,43277 ..43437,43824 ..4328,44069 ..44221, 44305 ..44408 .44502 ..44607,44691 ..44874,44972 ..45057, 45292 ..45357,45493 ..4550,45745 ..45885,46042 ..46119,45206 ..46328 .46511 ..4550,45745 ..45885,46042 ..46119,46206 ..46328 ..46511 ..46580 ..46882,46982 ..47093,47463 ..47681,47870 ..48243,48329 ..48479,48788 ..48823,48927 ..49132,49211 ..49316,49403 ..49696))
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complement(33893. .33928)
/rpt_family="\"
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/rpt_family="AT_rich"
complement(25863..36393)
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GEDMDIDVDKKPEQEKTEIVELDSPVSKTQRVLENKOEVEEEEKWEVEVESENKTKANVE
DKTQSIDRSMEETGDEPVNSAAEKLVVLASLEGPKSTQNEEEEEKEKRLQEQKKRLELE
RKEWRKKMQEKFQVRNPQLLSLCETLFPNDNHHSVWNGPHSLFRRRGGSNRSSALHK
AVESLMNELNNSLSYALGARSLFAMLDESGYFHTLRAATSNASIFIISTKAIGEYASL
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ATDTVKVQDVVYGQKDTKTSEENSQASKKAAELATISLOKEEKKTDQNLRYNKOELED
SLIVIKKIMKKEAADE RVPVNPEALGIPDYFDIIKTPMDFGTTCNNERKRIKKMNSE
DVYKDVNYIMNNCSKINKKGDYIVDLMKRVKKNEMKYWTSAGLYTEQSAAENTEDGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<40447. 40527,40617. 40739,40922. 410
41217. 41405,41490. 41576,41787. 41853,41997. 42067,
42272. 42409,42496. 42597,42686. 42596,4298. 43034,
43117. 43206,43297. 43437,43824. 43928,44069. 44221,
44305. 44408,44502. 44607,44691. 44874,44972. 45057,
45292. 45357,45493. 45550,45745. 45845,46042. 4419,
46206. 46328,46511. 46587,46594. 46882,46982. 47093,
46206. 46328,46511. 46587,46594. 46882,46982. 47033,
47463. 47681,47870. 48243,48399. 48479,48788. 48823,
48927. 49132,49211. 49316,49403. >496965))
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/gene="T15M6.6"
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AAVSIPVSPRRTKPTEEQRQSRSQSLLGVGMELWSPVAEIIRRSSEPSQCLVQSGDGA
/translation="MAPTKKPQKnKQSKNEIASSLIPNSGHKKPSKAPKLLISPENED
RLRRLLLNFRRTPSPVTATLSVTQKRKKLNNLYENLSCEGFLDNQIELVLSSLRDGAT
                                                          /product="hypothetical
/protein_id="AAG50700.1
/db_xref="GI:12321256"
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nplement(39499. .39523)
t_family="AT_rich"
94 .39704
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CDS

REFERENCE AUTHORS

Brassicales; Brassicaceae; 1 (bases 1 to 97146)

Palm, C.J., Conway, A.B.,

Conn, L.,

Arabidopsis.

SOURCE

ORGANISM

Arabidopsis thaliana

thale cress. AC007259.4

Eukaryota; Viridiplantae; Embryophyta; Trachec Magnoliophyta; eudicotyledons; core eudicots;

Tracheophyta; Spidicots; Rosidae;

Spermatophyta;

KEYWORDS ACCESSION

VERSION

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Matches 375; Conserv
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                                                                                                                 4496 tggataaagtcaatgaatgctgaactagagaaatttagatcaaaagatgtttacgaagaa 4555
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                                                                                                                                                                                                                                                                                                                                                                                                                            CATCAAGTGT - - CCATATGAGCATGCACTCTATATCAAAATTCAAAAAGAAGATATATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTCACTTCCAAATGGACACAAGGCAATTGGCGTGAAGTGGGTGTATAAAGCAAAGAAA 88671
                                                                                                                                                                                                                                                                      GAATTCAAGAAAGAGATGACGAAGGAGTTCGAGATGACGGACATTGGATTGATGTCTTAC
                                                                                                                                                                                                                                                                                                        aattttgtggatcaattgagagatcattttgaagttaaagtgtttggtgaaatatcaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                               actcaagttttacacaatgatggtttatttcacattgaatatgaagagggatcagtaata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTAGACTAATCATCTCACTAGCGGCTCAAAACAAGTGGAAGATACATCAAATGGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ataagattattgacaataataggttgtgaattaggaatgacaattcaacatttagacgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gttccaattcccaccggtgtgaagcctatatctatgggttggggtacatactgaggaaaatt 4615
                                                                                                                                                                                                                  tatcttggtattgaatttcgtaaaaccgaatctggttatattttatctcaagaaaaattt
                                                                                                                                                                                                                                                                                                                                                                      tatttaggtttatatgttgatgatattcttatggttggaagttcacaaaaagttattgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaacagtcgggtttggaatggtatcacactatcaaaagagtattggaagacattggtttt 4972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACATAGTCAAAGGTGAAGAAGACAAAGTCTTGAGACTAAAAAAGGCGCTTTATGGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCTCGGAATTGAAGTAAAACAAGAAGACAATGGAATATTCATAACTCAAGAAGGCTAT
                                                                                                                                                                                                                                                                                                                                                  ATCGCATGCTTATATGTAGATGACTTGATATTCACGGGTAACAATCCAAGCATGTTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAAGCCCCAAGAGCTTGGAAT-ACTCGAATTGACAAGTATTTCAAGGAGAAAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaatcagtacctttgaagaaaaaccattgttggttattgaaacgttctgtctatgggtta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTCGGCCTTCTTAAATGGAGATCTTGAAGAAGTTTACATTGAGCAACCACAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCCGGAATTGACTATGAC-----GAGGTATTTGCTCCCGTTGCTCGTCTAGAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aaggaaaaattggattatgacccttttagtgttagttcacctgttatagatcttgtgact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTCTAAAGGAGAAGTGGAAAGATACAAAGCAAGATTGGTTGCAAAAGGTTATAGTCAA
AC007259 97146 bp
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 chromosome I BAC T28P6
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Pred. No. 1.3e-06;
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 genomic sequence
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JOURNAL
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                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAMU BAC clone T19D16, gb|ATU95973.

e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described as
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'. The
software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E., Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-JUL-1999) DNA Sequencing and Technology Center,
Submitted University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
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Submitted (08-APR-1999) DNA Sequencing and Technology Center,
Submitted (O8-APR-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bases 90095-97146 of clone T28P6 overlap with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-AUG-1999) DNA Sequencing and Technology Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walker, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis, R.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 97146)
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FFSLGDSELRYVGIWYAQISQQTIVWVANRDHPINDTSGMVKFSNRGNLSVYASDNET
                                                                                                                                                                                              clone,
                                                                                                                                                                                                                                                                                               3106
                                                            /product="receptor-like protein kinase"
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                                                                                                                                                                                          /note="identical to cDNA receptor-like protein kinase clone, gi|4008007"
                                                                                                                                                                                                                                                                                                                      join(864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="I"
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                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="T28P6"
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                                                                                                                                                                                                                                                                                                                                                                                     /gene="T28P6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                              54. .2139,2289. .2408,2497. .2
.3343,3422. .3566,3650. .3964)
                                                                                                                                                                                                                                                                                                                      .2670,2798.
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bases 1-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanger Centre
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EVIITKLGLRIQEKGDVVRGAPVVQPGDDLFWFGKPRFILFLIHLVLFTNAFQLAFFA
                                     RKYIQRSLEKDFKTVVEISPVIWFVAVLFLLTNSYGLRSYLWLPFIPLVVILIVGTKL
                                                                                                                                                                                                                                                                                                                                                                                                multi-gene family in
                                                                                                                                                                                                                                                                                                                                                                                                                                 barley Mlo (control element of proteins, gi|1877221. One of s
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15263. 15323,15394. 15557,15641. 15735,15822. 15871,
15958. 15998,16078. 16251,16342. 16377,16463. 16530,
16620. 16680,16774. 17181)
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TFRKSNITASLAQSMSNVEVEQGLTAPNRCFRTFGQVTCHILRSLKLSLLGCHQVLTS
SSNLHSVGAITVPVSFLRRHTATEPEPSAPPLEMSRNMNHVSSSSIALKLDSLMDEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(9352. .10047,10150.
/gene="T28P6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(9352. .10839)
/gene="T28P6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHKEENNLNLLAYAWKLWNDGEAASLADPAVFDKCFEKEIEKCVHIGLLCVQEVANDR
PNVSNVIWMLTTENMSLADPKQPAFIVRRGASEAESSDQSSQKVSINDVSLTAVTGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APVIGVMLIAAVCVLLACRKYKKRPAPAKDRSAELMFKRMEALTSDNESASNQIKLKE
LPLFEFQVLATSTDSFSLRNKLGQGGFGPVYKGKLPEGQEIAVKRLSRKSGQGLEELM
NEVVVISKLOHRNLVKLLGCCIEGEERIDSRLKIIHRDLKASNILLDEKLNPKISDFG
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GNWSNGCMRKAPLQCERQRNVSNGGGGGKADGFLKLQKMKVPISAERSEASEQVCPKV
CLDNCSCTAYAYDRGIGCMLWSGDLVDMQSFLGSGIDLFIRVAHSELKTHSNLAVMIA
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PYDSFMPRWTLGTDGRTGGNLKLTSWTSHDDPSTGNYTAGIAPFTFPELLIWKNNYPT
WRSGPWNGQVFIGLPNMDSLLFLDGFNLNSDNQGTISMSYANDSFMYHFNLDPEGIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(4664. .4972,50
5661. .5821,5908. .6101,6189.
/gene="T28P6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4664. .7708)
/gene="T28P6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIFGGNQMEGCTSRVVGTFGYMAPEYAMEGQFSIKSDVYSFGVLMLEIITGKKNSAFH
EESSNLVGHIWDLWENGEATEIIDNLMDQETYDEREVMKCIQIGLLCVQENASDRVDM
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ASICSEKDGFVKLKRMKIPDTSDASVDMNITLKECKQRCLKNCSCVAYASAYHESKRG
AIGCLKWHGGMLDARTYLNSGQDFYIRVDKEELARWNRNGLSGKRRVLLILISLIAAV
                                                                               TSFGRRHLNFWSKTRVTLWTVCFFRQFFGSVTKVDYLALRHGFIMAHFAPGNESRFDF
                                                                                                                                                                                                                                                                               /protein_id="AAD49991.1"
/db_xref="GI:5734726"
                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T28P6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T28P6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLGGWIEIQNSREKQVKWSVSITDNPEDEVGWGMSVGGVVDGSRNHDQFQVESYLKFN
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ETLLCKSGIFRFGFFTPVNSTTRLRYVGIWYEKIPIQTVVWVANKDSPINDTSGVISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt SSVVIMLGHNATNLPNPKHPAFTSARRRGGENGACLKGQTGISVNDVTFSDIQGR"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRAELDWPKRMEIVRGIARGILYLHQDSRLRIIHRDLKASNILLDSEMIPKISDFGMA
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VAATNNFSSQNKLGAGRVTKPYGDSGEEVVEKLGTRNGRVQERGQADIKVAASKSHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEMPIGYIFUNSEVUNEDEVSFTYGVTDASVITRTMVNETGTMHRETWIARDKRWNDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Highly similar to Mlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGDRFRLSPCLVYHTNSDGRTIGLMLKSHWSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Hypothetical protein"
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/db_xref="GI:5734724"
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                                                                                                                                                                                                                                                                                                                                                                                                    . One of several members of arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4972,5054.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6296,6391.
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96,6391. .7708))
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                                                                                                                                                                                                                                                                                             acctgttatagatcttgtgactataagattattgacaataataggttgtgaattaggaat 4770
TTACATTGAGCAACCACAAGGCTACATAGTCAAAGGTGAAGAAGACAAAGTCTTGAGGCT 33907
                                                                                                                                                                       gacaattcaacatttagacgtcgagtcggcgtatctaaatgcctctattactcattcaaa 4830
                                                                                                                                                                                                                                                      TCCCGTTGCTCGTCTAGAAACGGTTAGACTAATCATCTCACTAGCGGCTCAAAACAAGTG
                                                                                                                                                                                                                                                                                                                                                                                   AAGATTGGTTGCAAAAGGTTATAGTCAAAGAGTCGGAATTGACTATGACGAGGTATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 tgttgtccatggcaacagacaaaaggaaaaattggattatgacccttttagtgttagttc 4710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTGGGTGTATAAAGCAAAGAAAAACTCT---AAAGGAGAAGTGGAAAGATACAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAAAAGAATGACACATGGGAGTTAACTTCACTTCCAAATGGACACAAGGCAATTGGCCGT 34204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAAAGCCATTGAAAAGAAGACTTGGAGAAATGCCATGGATGAAGAGATCAAATCAAT 34264
                                                           tccaatttatgtctttcctcctaaatcagtacctttgaagaaaaaccattgttggttatt 4890
                                                                                                                            GAAGATACATCAAATGGATGTCAAGTCGGCCTTCTTAAATGGAGATCTTGAAGAAGAAGT 33967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375;
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sprifregefsvnstryagimynsipvoltvlwankdpindssgvisisedgnlv
vtdgorvlwstarsanktyrabellesgklulkoantdaylwesfryptdswlpn
MLVGTNARTGGGNITITSWINDSDPSPGSYTAALVLAPYPLEIFINNDNNATWRSG
MUKGTNARTGGGNITITSWINDSDPSPGSYTAALVLAPYPLEIFINNDNNATWRSG
EMMGLMFNGLEDVYPGLFLYREKVNDDINGSAIMSYAADSTLAHLYLDYRGFAIRRDW
SEARRNWILGSQVPATECDIYSRCGQVTTCNPRKNPHCSCIKGFRPRNLIEWNNGNMS
GGCIRKLPLQCERQNNKGSADRELKLORMKMDDFARRSEASEPECFMTCLGSCSCIAF
AHGLOYGCMINNESLVDSQVLSASGNDLSIRLAHSEKTODRRPILIGTSLAGGIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTDGQRRVLWSTNVSTQASANSTVAELLDSGNLVLKEASSDAYLWESFKYPTDSWLPN
MLVGTNARIGGGNVTITSWKSPSDPSPGSYTAALVLAAYPELFIMNNNNNNSTVWRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MRLHESSSPFVCILVLSCFFLSVSLAQERAFFSGKLNDSETIVS
SFRTFRFGFFSPVNSTSRYAGIWYNSVSVQTVIWVANKDKPINDSSGVISVSQDGNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(20734. .21042,21122. .21251,21332. .21569
21652. .21862,21947. .22125,22207. .22314,22404. .23691))
/gene="T28P6.6"
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FSLSNKLGQGGFGPVYKGMLLEGQEIAVKRLSQASGQGLEELVTEVVVISKLQHRNLV
KLFGCCIAGEERMLVVEFMPKKSLDFYIFDPREAKLLDWNTRFEIINGICRGLLYLHR
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18284. .18494,18566. .18744,18826. ..)
/gene="T28P6.5"
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AMGGLFSEKSDVFSLGVILLEIISGRRNSHSTLLAHVWSIWNEGEINGMVDPEIFDQL
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SSPSPRYSGHGHHEHQFWDPESQHQEAETSTHHSLAHESSEPVLASVELPPIRTSKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAD49993.1"
/db_xref="GI:5734728"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEKEIRKCVHIALLCVQDAANDRPSVSTVCMMLSSEVADIPEPKQPAFMPRNVGLEAE
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/db_xref="GI:5734727"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
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.18933,19024. .20311))
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                                                                                                                                                                                                                LTR
                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAT 33546
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-SEP-1996) C. Herve, INRA-CNRS, LBMRPM, Chemin De Borde Rouge Bp27, Castanet-Tolosan Cedex, 31326, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 4793)
Herve,C., Serres,J., Dabos,P. and Lescure,B.
Nucleotide sequence of DNA art1 (accession no. Y08010), a new
Arabidopsis copia-like transposable element, disrupts a lectin
receptor kinase gene in the columbia ecotype (PGR97-059)
Plant Physiol. 113, 1464-1464 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots, Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.thaliana lectin receptor kinase y08010
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Overlaps with Y08020.
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                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                   /lab_host="EMBL-3 CLONTECH"
                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
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Best Local S
Matches 374
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Local Similarity 49.1%;
hes 374; Conservation
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YHYIRECVSKKDVQLEYVKTHDQVADIFTKPLKREDFIKMRSLLGVAKSSLRGGVES"
4354. _4793
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TKVPMSKNRMFYLNIRNDIAQCLKMCYKEESWLWHLRFGHLNFGGLELLSRKEMVRGL
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YEHALY IK IQK EDILI ACLYVDDLI FTGNNPSMFEEFKKEMTKEFEMTD IGLMSYYLG
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ERYKARLVAKGYSQRAGIDYDEIFAFVARLETVRLIISLAAQNKWKIHQMDVKSAFLN
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REEPPSEEPTTPPTSPTSSQIEESSSERTPRFRSIQELYEVTENQENLTLFCLFAECE
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Pred. No. 3.4e-06;
0; Mismatches 376;
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3728 GCTAAGGAGGTACTTAAGAAGTTCAAGATGGATGACTCAAAT 3769
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